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OM protein - protein search, using sw model

Run on: June 3, 2005, 14:38:59 ; Search time 142 Seconds
(without alignments)
837.422 Million cell updates/sec

Perfect score: 1806
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Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 1465611

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1060	225.5	12.5	869	16	US-10-471-115-18	Sequence 18, Appl
1061	224.5	12.4	477	15	US-10-613-413A-23	Sequence 23, Appl
1062	224.5	12.4	477	17	US-10-885-225-23	Sequence 23, Appl
1063	224.5	12.4	477	17	US-10-954-094-23	Sequence 23, Appl
1064	224.5	12.4	869	9	US-09-817-487A-2	Sequence 2, Appl
1065	224.5	12.4	1171	15	US-10-435-751-5	Sequence 5, Appl
1066	224.5	12.4	1171	15	US-10-435-751-21	Sequence 21, Appl
1067	224.5	12.4	1171	15	US-10-435-751-154	Sequence 154, App
1068	224.5	12.4	1171	15	US-10-435-751-156	Sequence 156, App
1069	224.5	12.4	1171	15	US-10-435-751-200	Sequence 200, App
1070	224.5	12.4	1224	15	US-10-435-751-30	Sequence 30, Appl
1073	224	12.4	1059	9	US-09-905-291A-290	Sequence 290, App
1141	224	12.4	1059	14	US-10-289-976-290	Sequence 290, App
1142	224	12.4	1059	14	US-10-289-937-290	Sequence 290, App
1143	224	12.4	1059	15	US-10-298-923-290	Sequence 290, App
1144	224	12.4	1059	15	US-10-448-923-290	Sequence 290, App
1145	224	12.4	1059	15	US-10-449-656-290	Sequence 290, App
1146	224	12.4	1059	15	US-10-448-713-290	Sequence 290, App
1147	224	12.4	1059	15	US-10-425-447-290	Sequence 290, App
1148	224	12.4	1059	16	US-10-215-371-290	Sequence 290, App
1149	224	12.4	1059	16	US-10-771-187-290	Sequence 290, App
1150	224	12.4	1059	17	US-10-963-467-290	Sequence 290, App
1151	224	12.4	1059	17	US-10-978-355-290	Sequence 290, App
1154	224	12.4	1119	9	US-09-905-291A-294	Sequence 294, App

Search completed: June 3, 2005, 14:53:32
Job time : 164 secs

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OM protein - protein search, using sw model

Run on: June 3, 2005, 14:25:22 ; Search time 175 Seconds
(without alignments)
1006.601 Million cell updates/sec

Title: US-09-978-544a-523
Perfect score: 1806
Sequence: 1 MKTIQPMKNSISWAFITGL.....RRAGCWLPPLVHLILKE 344

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1500 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1780	98.6	344	2	Q8BG33
2	1665.5	92.2	344	1	NTRI_HUMAN
3	1647.5	91.2	344	1	NTRI_MOUSE
4	1639.5	90.8	344	1	NTRI_RAT
5	1477.5	81.8	353	1	CEPU_CHICK
6	1428	79.1	313	2	OS7596
7	1427.5	79.0	344	2	OS3242
8	1357.5	75.2	315	2	OSD615
9	1306	72.3	337	2	OSD6F2
10	1305	72.3	337	1	OSCM_CHICK
11	1295.5	71.7	338	2	Q7Z3W6
12	1275.5	70.7	345	2	OSGM08
13	1275.5	70.6	344	2	Q9DF61
14	1270.5	70.3	344	2	OSB014
15	1268	70.2	345	1	OSCM_HUMAN
16	1266	70.1	345	1	OSCM_BOVIN
17	1259	69.7	345	1	OSCM_RAT
18	993.5	55.0	342	2	OS42G9
19	946	52.4	334	2	OS2870
20	938.5	52.0	338	1	LAMP_CHICK
21	931.5	51.6	338	1	LAMP_HUMAN
22	930.5	51.5	350	2	OS2869
23	926.5	51.3	338	2	LAMP_RAT
24	904	50.1	337	2	OS61Z7
25	894	49.5	341	1	LAMP_MOUSE
26	842	46.6	352	2	OSW6V2
27	823	45.6	352	1	NEGR_HUMAN
28	815	45.1	348	1	NEGR_RAT
29	814	45.1	348	1	NEGR_MOUSE
30	759	42.0	325	2	OSHW98
31	686.5	38.0	188	2	OSBMT5

32	656.5	36.4	262	2	Q80T70	Q80T70 mus muscu
33	599	33.2	261	2	Q9W6V1	Q9W6V1 gallus gall
34	545.5	30.2	226	2	Q8N440	Q8N440 homo sapien
35	380.5	21.1	606	2	Q9VMN6	Q9VMN6 drosophila
36	367	20.3	303	2	Q7Q154	Q7Q154 anopheles g
37	359.5	19.9	299	2	Q7Q863	Q7Q863 anopheles g
38	358	19.8	320	2	Q7Q0P8	Q7Q0P8 anopheles g
39	350.5	19.4	672	2	Q81P70	Q81P70 drosophila
40	349.5	19.4	532	2	Q6NMJ3	Q6NMJ3 drosophila
41	349.5	19.4	532	2	Q9VLE0	Q9VLE0 drosophila
42	348	19.3	554	2	Q9W4R3	Q9W4R3 drosophila
43	346	19.2	301	2	Q7Q864	Q7Q864 anopheles g
44	341	18.9	316	2	Q7Q0P9	Q7Q0P9 anopheles g
45	338.5	18.7	413	2	Q9VAR6	Q9VAR6 drosophila
46	338	18.7	299	2	Q7Q8F3	Q7Q8F3 anopheles g
47	333	18.4	315	2	Q9VMB2	Q9VMB2 drosophila
48	328	18.2	399	2	Q7QCH7	Q7QCH7 anopheles g
49	318	17.6	340	2	Q7Q807	Q7Q807 anopheles g
50	313	17.3	550	2	Q9VMN9	Q9VMN9 drosophila
51	312.5	17.3	285	2	Q7PN14	Q7PN14 anopheles g
52	308.5	17.1	528	2	P91670	P91670 drosophila
53	306	16.9	545	2	Q9VCT4	Q9VCT4 drosophila
54	305	16.9	413	2	Q7Q8V2	Q7Q8V2 anopheles g
55	303.5	16.8	316	2	Q8WPE3	Q8WPE3 drosophila
56	300.5	16.6	316	2	Q8WP94	Q8WP94 drosophila
57	299	16.6	948	2	Q9VME2	Q9VME2 drosophila
58	299	16.6	401	2	Q7PSS8	Q7PSS8 anopheles g
59	297.5	16.5	316	2	Q8WPE8	Q8WPE8 drosophila
60	297.5	16.5	333	1	AMAL_DROME	AMAL_DROME drosophila
61	297.5	16.5	341	2	Q7K5X2	Q7K5X2 drosophila
62	294.5	16.3	383	2	Q7Q8C5	Q7Q8C5 anopheles g
63	292.5	16.2	333	2	Q7PXA4	Q7PXA4 anopheles g
64	290.5	16.1	2673	2	Q96SC3	Q96SC3 homo sapien
65	290.5	16.1	5636	2	Q96RW7	Q96RW7 homo sapien
66	287	15.9	846	2	Q57577	Q57577 cyrops pyrr
67	287	15.9	1100	2	Q57576	Q57576 cyrops pyrr
68	285.5	15.8	603	2	Q9NKE5	Q9NKE5 anopheles g
69	285.5	15.8	403	2	Q9VPO8	Q9VPO8 drosophila
70	284	15.7	725	1	NCA2_MOUSE	NCA2_MOUSE mus muscu
71	283.5	15.7	1115	1	NCA1_MOUSE	NCA1_MOUSE mus muscu
72	283.5	15.6	605	2	Q921P2	Q921P2 mus muscu
73	282.5	15.6	838	2	Q8BQ96	Q8BQ96 mus muscu
74	282.5	15.6	838	2	Q8C4B2	Q8C4B2 mus muscu
75	279.5	15.5	725	1	Q73633	Q73633 xenopus lae
76	279.5	15.5	1091	1	NCA1_CHICK	NCA1_CHICK gallus gall
77	279.5	15.5	725	2	Q98918	Q98918 gallus gall
78	278.5	15.4	4162	2	Q661V0	Q661V0 xenopus lae
79	277.5	15.4	719	2	NCA1_RAT	NCA1_RAT rattus norv
80	277.5	15.4	858	1	NCA1_XENILA	NCA1_XENILA xenopus lae
81	277.5	15.4	1088	1	Q6PFR4	Q6PFR4 brachydantio
82	276.5	15.3	405	2	Q6PFR4	Q6PFR4 brachydantio
83	276	15.3	761	1	NCA2_HUMAN	NCA2_HUMAN homo sapien
84	276	15.3	848	1	NCA1_HUMAN	NCA1_HUMAN homo sapien
85	275.5	15.3	853	1	NCA1_BOVIN	NCA1_BOVIN bos taurus
86	273.5	15.1	725	1	Q73634	Q73634 xenopus lae
87	272.5	15.1	433	2	Q6DU83	Q6DU83 xenopus tro
88	272.5	15.1	1323	2	Q88476	Q88476 gallus gall
89	271	15.0	858	2	Q86X47	Q86X47 homo sapien
90	270.5	15.0	1092	1	NCA2_XENILA	NCA2_XENILA xenopus lae
91	270	14.9	1479	2	Q7KQ75	Q7KQ75 drosophila
92	269.5	14.9	484	2	Q26475	Q26475 histiocerc
93	268.5	14.9	1496	2	Q92626	Q92626 homo sapien
94	265	14.7	392	2	Q7PSS2	Q7PSS2 anopheles g
95	265	14.7	1482	2	Q9V4Y0	Q9V4Y0 drosophila
96	264.5	14.6	1185	2	Q7PRK4	Q7PRK4 anopheles g
97	263	14.6	316	2	Q7Q8A7	Q7Q8A7 anopheles g
98	263	14.6	1431	2	Q80U60	Q80U60 mus muscu
99	263	14.6	3950	2	Q7YRFS	Q7YRFS canis fami
100	261.5	14.5	437	2	Q81ZP8	Q81ZP8 homo sapien
101	261.5	14.5	1010	1	CONT_CHICK	CONT_CHICK gallus gall
102	261	14.5	1031	2	Q90T82	Q90T82 brachydantio
103	261	14.5	1395	2	Q44924	Q44924 drosophila
104	261	14.5	3410	2	Q7TND0	Q7TND0 rattus norv

105	260.5	14.4	500	2	Q9W260	Q9W260 drosophila	178	229.5	12.7	869	1	MUSK_HUMAN	O15146 homo sapien
106	260.5	14.4	500	2	Q9X2B7	Q9X2B7 drosophila	179	229	12.7	1056	2	Q9O203	Q9O203 xenopus lae
107	260	14.4	601	2	Q96CJ3	Q96CJ3 homo sapien	180	229	12.7	4391	1	PGBM_HUMAN	P98160 homo sapien
108	260	14.4	1395	2	Q7KVX3	Q7KVX3 drosophila	181	228.5	12.7	1040	2	Q9W675	Q9W675 brachydantio
109	260	14.4	1429	2	Q9W213	Q9W213 drosophila	182	228.5	12.7	1117	2	O6PIC6	O6PIC6 mus musculu
110	259	14.3	7962	2	O10465	O10465 homo sapien	183	228	12.6	1028	2	O8CCK1	O8CCK1 mus musculu
111	259	14.3	34350	2	Q8W242	Q8W242 homo sapien	184	227.5	12.6	1051	1	P7K7_CHICK	P91048 gallus gall
112	258.5	14.3	395	2	Q8BXJ7	m mus muscu	185	227.5	12.6	1059	2	P97527	P97527 rattus norv
113	258.5	14.3	395	2	Q8BZP4	Q8BZP4 mus musculu	186	227	12.6	1189	2	Q9P2J2	Q9P2J2 homo sapien
114	258.5	14.3	404	2	Q8BLQ9	Q8BLQ9 mus musculu	187	226.5	12.5	476	2	O6APY5	O6APY5 rattus norv
115	258.5	14.3	404	2	Q8BYP1	Q8BYP1 mus musculu	188	226	12.5	6632	1	UN89_CABRL	O01761 caenorhabdi
116	257	14.2	1056	2	Q7ZW34	Q7ZW34 brachydantio	189	225	12.5	8081	2	Q7Z120	Q7Z120 caenorhabdi
117	256	14.2	435	2	Q8N3T6	Q8N3T6 homo sapien	190	225.5	12.5	868	1	MUSK_MOUSE	O61006 mus musculu
118	255.5	14.1	838	2	Q90YML	Q90YML brachydantio	191	225.5	12.5	1388	2	Q7QKD0	Q7QKD0 anopheles g
119	255	14.1	359	2	LACH_DROME	Q24372 drosophila	192	225.5	12.5	1662	2	Q7Q1V4	Q7Q1V4 anopheles g
120	255	14.1	359	2	Q9V6C2	Q9V6C2 drosophila	193	224.5	12.4	1224	2	O00533	O00533 homo sapien
121	254.5	14.1	5175	2	O810L3	O810L3 caenorhabdi	194	224	12.4	330	2	Q9H1X9	Q9H1X9 homo sapien
122	254.5	14.1	5198	2	Q76518	Q76518 caenorhabdi	195	224	12.4	697	2	O8NC72	O8NC72 homo sapien
123	251.5	13.9	837	1	NCM2_MOUSE	O35136 mus musculu	196	224	12.4	1059	2	O6UXJ7	O6UXJ7 homo sapien
124	250.5	13.9	1342	2	Q9GPE6	Q9GPE6 drosophila	197	224	12.4	1119	2	O6UXM1	O6UXM1 homo sapien
125	250.5	13.9	1342	2	Q9VP27	Q9VP27 schistocerc	198	224	12.4	1252	2	Q96DN3	Q96DN3 homo sapien
126	250	13.8	349	1	LACH_SCHAM	Q6474 schistocerc	199	223	12.3	417	2	Q7TNL1	Q7TNL1 mus musculu
127	250	13.8	525	2	Q7PZS8	Q7PZS8 anopheles g	200	222	12.3	450	2	Q9VR25	Q9VR25 drosophila
128	250	13.8	795	2	Q90YMO	Q90YMO brachydantio	201	222	12.3	595	2	O6ZRS5	O6ZRS5 homo sapien
129	250	13.8	955	1	MDG1_HUMAN	Q9HYP4 homo sapien	202	221.5	12.3	862	1	CD22_MOUSE	P35329 mus musculu
130	249.5	13.8	1040	1	AXO1_HUMAN	Q02246 homo sapien	203	221	12.2	435	2	Q8WR44	Q8WR44 caenorhabdi
131	246.5	13.6	627	2	Q8N466	Q8N466 homo sapien	204	221	12.2	436	2	O8MPV1	O8MPV1 caenorhabdi
132	246.5	13.6	727	2	O6RKX2	O6RKX2 rattus norv	205	221	12.2	1340	2	O8NDA2	O8NDA2 homo sapien
133	246.5	13.6	837	2	O6RKX3	O6RKX3 rattus norv	206	221	12.2	1746	2	O8WY19	O8WY19 homo sapien
134	246.5	13.6	865	2	O68DA2	O68DA2 homo sapien	207	221	12.2	1827	2	O9VSG5	O9VSG5 drosophila
135	246.5	13.6	1018	1	CONT_HUMAN	Q12860 homo sapien	208	221	12.2	2012	1	DSCA_HUMAN	O60469 homo sapien
136	245.5	13.6	1065	1	LIG2_HUMAN	Q4898 homo sapien	209	220.5	12.2	333	2	O86WB8	O86WB8 homo sapien
137	245	13.6	1028	2	O6INB5	O6IND8 xenopus lae	210	220.5	12.2	336	2	Q80VQ4	O80VQ4 mus musculu
138	244.5	13.5	512	2	Q96DM8	Q96DM8 homo sapien	211	220.5	12.2	336	2	Q9DEB7	Q9DEB7 mus musculu
139	243.5	13.5	837	2	Q7Z7F2	Q7Z7F2 homo sapien	212	220.5	12.2	488	2	O6FJ33	O6FJ33 mus musculu
140	243.5	13.5	949	1	MDC1_MOUSE	PE0755 mus musculu	213	220.5	12.2	443	2	O8NZF4	O8NZF4 homo sapien
141	243.5	13.5	956	1	MDC1_HUMAN	Q7Z553 homo sapien	214	220.5	12.2	445	2	O8K3T6	O8K3T6 mus musculu
142	243.5	13.5	1021	1	CONT_RAT	O63198 rattus norv	215	220.5	12.2	445	2	O8R4L1	O8R4L1 mus musculu
143	243.5	13.5	1036	1	AXO1_CHICK	P28685 gallus gall	216	220.5	12.2	456	2	O8R5M8	O8R5M8 mus musculu
144	242.5	13.4	949	1	MDCL_RAT	PE0756 rattus norv	217	220.5	12.2	898	1	FAS2_SCHAM	P22648 schistocerc
145	242.5	13.4	1020	2	O6NXY7	O6NXY7 mus musculu	218	220	12.2	1043	2	Q6PA07	Q6PA07 xenopus lae
146	241.5	13.4	837	1	NCM2_HUMAN	O15194 homo sapien	219	220	12.2	1614	2	O8UYD7	O8UYD7 xenopus lae
147	241.5	13.4	1018	2	Q28106	Q28106 bos taurus	220	219.5	12.2	330	2	Q90Z42	Q90Z42 gallus gall
148	241.5	13.4	1020	1	CONT_MOUSE	P12960 mus musculu	221	219.5	12.2	330	2	O66KX2	O66KX2 xenopus lae
149	240.5	13.3	757	2	Q7QCU0	Q7QCU0 anopheles g	222	219.5	12.2	442	2	O9BY67	O9BY67 homo sapien
150	240	13.3	3707	1	PGBM_MOUSE	O05793 mus musculu	223	219.5	12.1	1009	2	O93250	O93250 xenopus lae
151	237.5	13.2	702	2	O69ZT8	O69ZT8 mus musculu	224	219	12.1	1026	2	O8IWW2	O8IWW2 homo sapien
152	237	13.1	312	2	O66KV0	O66KV0 xenopus lae	225	219	12.1	1062	2	O8BKX3	O8BKX3 mus musculu
153	235.5	13.0	632	2	O6ZRX5	O6ZRX5 homo sapien	226	219	12.1	1081	1	LIG1_MOUSE	P70193 mus musculu
154	235.5	13.0	1027	2	Q90W79	Q90W79 gallus gall	227	219	12.1	1093	1	LIG1_HUMAN	Q96141 homo sapien
155	235.5	13.0	2623	2	Q6WR10	O6WR10 homo sapien	228	218.5	12.1	1114	2	Q9BWW1	O9BWW1 homo sapien
156	234.5	13.0	358	2	Q90490	Q90490 brachydantio	229	218.5	12.1	1115	2	O6UXJ5	O6UXJ5 homo sapien
157	234.5	13.0	779	2	O97136	O97136 manduca sex	230	218.5	12.1	1115	2	O6UXJ5	O6UXJ5 homo sapien
158	234.5	13.0	837	2	O97137	O97137 manduca sex	231	218.5	12.1	1612	1	ROB1_MOUSE	O89026 mus musculu
159	234.5	13.0	1040	1	AXO1_RAT	P22063 rattus norv	232	218	12.1	705	2	O8C5D3	O8C5D3 mus musculu
160	233.5	12.9	1026	2	O94780	O94780 homo sapien	233	218	12.1	2013	2	O8VHZ8	O8VHZ8 rattus norv
161	233.5	12.9	1100	2	O94779	O94779 homo sapien	234	218	12.1	2013	2	Q9ERC8	Q9ERC8 mus musculu
162	233	12.9	394	2	Q7ZXX1	Q7ZXX1 xenopus lae	235	217.5	12.0	348	2	O00557	O00557 homo sapien
163	233	12.9	1028	2	P97528	P97528 rattus norv	236	217.5	12.0	1555	2	Q7PZH8	Q7PZH8 anopheles g
164	232.5	12.9	2693	2	O8ISF3	O8ISF3 caenorhabdi	237	217	12.0	885	2	O8HYV1	O8HYV1 sus scrofa
165	232.5	12.9	2708	2	O8ISF4	O8ISF4 caenorhabdi	238	217	12.0	886	2	O8HYV2	O8HYV2 sus scrofa
166	232.5	12.9	18519	2	O8ISF6	O8ISF6 caenorhabdi	239	217	12.0	1443	2	O8MTB2	O8MTB2 drosophila
167	232.5	12.9	18534	2	O8ISF7	O8ISF7 caenorhabdi	240	217	12.0	1765	2	O9VTS0	O9VTS0 drosophila
168	231.5	12.8	858	2	O18466	O18466 hirudo medi	241	217	12.0	1170	2	O9V829	O9V829 drosophila
169	231.5	12.8	1005	2	P79921	P79921 xenopus lae	242	216.5	12.0	1109	2	O6P5H3	O6P5H3 mus musculu
170	231	12.8	703	2	Q21139	Q21139 caenorhabdi	243	215.5	11.9	286	2	Q7PE93	Q7PE93 anopheles g
171	231	12.8	1028	2	Q9UQ52	Q9UQ52 homo sapien	244	215.5	11.9	497	2	Q9BXN7	Q9BXN7 homo sapien
172	231	12.8	1028	2	Q9JMB8	Q9JMB8 mus musculu	245	215.5	11.9	714	2	O6ZPE6	O6ZPE6 mus musculu
173	230.5	12.8	807	2	Q6N2Y3	O6N2Y3 brachydantio	246	215.5	11.9	886	2	Q9VM64	Q9VM64 drosophila
174	230.5	12.8	868	1	Q6N2Y3	O6N2Y3 rattus norv	247	215.5	11.9	1302	1	NRG_DROME	P20241 drosophila
175	230.5	12.8	1032	2	O8UVD6	O8UVD6 brachydantio	248	215.5	11.9	2597	2	O6WTH9	O6WTH9 rattus norv
176	229.5	12.7	510	2	AXO1_MOUSE	O61330 mus musculu	249	215	11.9	443	2	O8WR43	O8WR43 caenorhabdi
177	229.5	12.7	510	2	O801V8	O801V8 brachydantio	250	215	11.9	444	2	O8WPU9	O8WPU9 caenorhabdi

251	215	11.9	789	2	Q7PME2	Q7PME2 anophelae g	324	202	11.2	1269	2	001632	001632 caenorhabdi
252	215	11.9	1419	2	Q98SW3	Q98sw3 brachydantio	325	202	11.2	1273	2	044928	044928 caenorhabdi
253	214.5	11.9	816	2	Q98FAS	Q98fas homo sapien	326	202	11.2	1409	2	08J127	08J127 brachydantio
254	214.5	11.9	1070	2	Q6IQ54	Q6iq54 homo sapien	327	202	11.2	1409	2	0801M2	0801m2 brachydantio
255	214.5	11.9	1651	1	ROBI_RAT	055005 rattus norv	328	202	11.2	1428	2	08A167	08A167 brachydantio
256	214	11.8	240	2	Q7PRJ5	Q7prt5 anophelae g	329	202	11.2	2022	2	07K0G5	07Kqg5 drosophila
257	214	11.8	498	2	Q8BRJ5	Q8brt6 mus musculu	330	201.5	11.2	388	2	08NF28	08nf28 homo sapien
258	213.5	11.8	391	2	Q7QJG1	Q7qjg1 anophelae g	331	201.5	11.2	771	2	07QEF8	Q7qef8 anophelae g
259	213.5	11.8	398	2	Q8N126	Q8n126 homo sapien	332	201.5	11.2	2008	2	09VEJ5	Q9vej5 drosophila
260	213.5	11.8	920	2	Q9P232	Q9p232 homo sapien	333	201.5	11.2	2046	2	07KSR9	Q7ksr9 drosophila
261	213.5	11.8	1389	2	Q90Z69	Q9p269 brachydantio	334	201.5	11.2	3215	2	08IRV7	Q8irv7 drosophila
262	213	11.8	484	2	Q6BE00	Q6be00 xenopus lae	335	201.5	11.2	3262	2	09EQJ5	Q9eqj5 mus musculu
263	213	11.8	898	2	Q69Z26	Q69z26 mus musculu	336	201.5	11.2	4117	2	08IRV9	Q8irv9 drosophila
264	213	11.8	1134	2	Q71B05	Q71b05 brachydantio	337	201.5	11.2	4179	2	08M4Y4	Q8m4y4 drosophila
265	212.5	11.8	1264	2	P91767	P91767 manduca sex	338	201.5	11.2	4223	2	08MPY3	Q8mpy3 drosophila
266	212	11.7	1026	2	Q6Z845	Q6z845 rattus norv	339	201.5	11.2	4228	2	08IRV8	Q8irv8 drosophila
267	212	11.7	1151	2	Q9QVNS	Q9qvn5 rattus sp.	340	201.5	11.2	8647	2	Q7KOP5	Q7kqp5 drosophila
268	211.5	11.7	382	2	Q7PSH7	Q7psh7 anophelae g	341	201.5	11.2	8930	2	Q7KOP7	Q7kqp7 drosophila
269	211.5	11.7	749	2	Q7Q6H1	Q7q6h1 anophelae g	342	201.5	11.2	8943	2	Q9V4F7	Q9v4f7 drosophila
270	211.5	11.7	873	1	FAS2_DROME	P34082 drosophila	343	201	11.1	487	2	Q7T2H2	Q7t2h2 gallus gall
271	211.5	11.7	1070	1	PKT7_HUMAN	O13308 homo sapien	344	201	11.1	623	2	08BY18	Q8by18 mus musculu
272	211.5	11.7	1102	2	Q923F7	Q923f7 mus musculu	345	201	11.1	688	2	Q80Z53	Q80z53 mus musculu
273	211.5	11.7	1109	2	Q8CE91	Q8ce91 mus musculu	346	201	11.1	700	1	KIR2_MOUSE	KIR2_MOUSE mus musculu
274	211.5	11.7	1109	2	Q6AZB0	Q6azb0 mus musculu	347	201	11.1	946	2	007153	007153 torpedo cal
275	211.5	11.7	1110	2	Q8CE73	Q8ce73 mus musculu	348	201	11.1	1709	1	SN_HUMAN	SN_HUMAN mus musculu
276	211.5	11.7	1461	1	NEOI_HUMAN	Q92859 homo sapien	349	201	11.1	1735	2	Q7Q916	Q7q916 anophelae g
277	211.5	11.7	1461	1	Q7QJ39	Q7qj39 anophelae g	350	200.5	11.1	1085	2	Q7OH02	Q7oh02 anophelae g
278	211	11.7	366	2	Q99N28	Q99n28 m hecctin-11	351	200.5	11.1	1271	2	Q6U714	Q6u714 brachydantio
279	211	11.7	6620	2	Q96AA2	Q96aa2 homo sapien	352	200.5	11.1	1447	1	DCQ_MOUSE	DCQ_MOUSE mus musculu
280	210	11.6	1561	2	Q924D2	Q924d2 mus musculu	353	200.5	11.1	1493	1	NEOI_MOUSE	NEOI_MOUSE mus musculu
281	210	11.6	1730	2	Q7YRQ7	Q7yrq7 sus scrofa	354	200.5	11.1	5516	2	Q7Z248	Q7z248 brachydantio
282	210	11.6	1914	1	KMLS_HUMAN	O15746 homo sapien	355	199.5	11.0	1445	2	Q63155	Q63155 rattus norv
283	210	11.6	1914	2	Q7Z4T0	Q7z4t0 homo sapien	356	199.5	11.0	1465	2	Q7TQG5	Q7tqg5 mus musculu
284	210	11.6	1940	2	Q6PDV3	Q6pdv3 mus musculu	357	199	11.0	440	2	Q6ZMD4	Q6zmd4 homo sapien
285	209	11.6	504	2	Q8N441	Q8n441 homo sapien	358	199	11.0	940	2	Q8NFA7	Q8nfa7 homo sapien
286	209	11.6	504	2	Q9H4D7	Q9h4d7 homo sapien	359	199	11.0	1241	1	NPHN_HUMAN	NPHN_HUMAN mus musculu
287	209	11.6	1030	2	Q8NFA8	Q8nfa8 homo sapien	360	199	11.0	1513	2	Q90Z70	Q90z70 brachydantio
288	209	11.6	1030	2	Q7OEG7	Q7oeg7 homo sapien	361	199	11.0	1723	2	Q8CHB2	Q8chb2 mus musculu
289	208	11.5	1028	2	Q07409	Q07409 mus musculu	362	198.5	11.0	931	2	Q6KAMS	Q6kams mus musculu
290	208.5	11.5	1651	1	ROBI_HUMAN	Q9y6n7 homo sapien	363	198.5	11.0	2053	2	Q81Z14	Q81zy4 homo sapien
291	208	11.5	1155	2	Q7Q3K8	Q7q3k8 anophelae g	364	198	11.0	437	2	Q86YV1	Q86yv1 homo sapien
292	207.5	11.5	1329	2	Q8N225	Q8n225 homo sapien	365	198	11.0	662	2	Q609Z6	Q609z6 homo sapien
293	207.5	11.5	1643	2	Q7QGT8	Q7qgt8 anophelae g	366	198	11.0	847	1	Q9NEG0	Q9neg0 drosophila
294	207	11.5	600	2	Q8N7W7	Q8n7w7 homo sapien	367	198	11.0	907	2	Q9NEG0	Q9neg0 drosophila
295	206.5	11.4	915	2	Q8R4B3	Q8r4b3 mus musculu	368	198	11.0	1240	1	NPAS_RAT	NPAS_RAT mus musculu
296	206.5	11.4	2016	2	Q9NBA1	Q9nba1 drosophila	369	197.5	10.9	1164	2	Q66MNS	Q66mns drosophila
297	206	11.4	1187	2	Q8WR45	Q8wr45 caenorhabdi	370	197.5	10.9	1228	2	Q8MRA3	Q8mra3 drosophila
298	205.5	11.4	1028	2	Q6Z682	Q6z682 rattus norv	371	197.5	10.9	1235	2	Q86BD5	Q86bd5 drosophila
299	205.5	11.4	2016	2	Q8MKM6	Q8mkm6 drosophila	372	197.5	10.9	1235	2	Q9V787	Q9v787 drosophila
300	205.5	11.4	2016	2	Q8MKM7	Q8mkm7 drosophila	373	197.5	10.9	1240	1	NPAS_MOUSE	NPAS_MOUSE mus musculu
301	205.5	11.4	2019	2	Q8MKM8	Q8mkm8 drosophila	374	197.5	10.9	1251	2	Q6ZD54	Q6zds4 mus musculu
302	205.5	11.4	17352	2	Q95YM2	Q95ym2 procambartus	375	197.5	10.9	1447	1	DCQ_HUMAN	DCQ_HUMAN mus musculu
303	205	11.4	433	2	Q9UJY1	Q9ujy1 homo sapien	376	197.5	10.9	16215	2	Q9NFS3	Q9nfs3 drosophila
304	204.5	11.3	439	2	Q57349	Q57349 gallus galli	377	197.5	10.9	18074	2	Q917U4	Q917u4 drosophila
305	204.5	11.3	1377	1	NEOI_RAT	P97603 rattus norv	378	197	10.9	537	2	Q7PSJ8	Q7psj8 anophelae g
306	204.5	11.3	1675	2	Q98SM4	Q98sm4 brachydantio	379	196	10.9	1240	1	NPAS_HUMAN	NPAS_HUMAN mus musculu
307	204.5	11.3	3197	2	Q9W1D5	Q9w1d5 drosophila	380	196	10.9	1906	1	KMLS_CHICK	KMLS_CHICK mus musculu
308	204	11.3	430	2	Q7Q3S8	Q7q3s8 anophelae g	381	195.5	10.8	1270	2	Q9U3F2	Q9u3f2 caenorhabdi
309	204	11.3	1443	1	NEOI_CHICK	Q9g610 gallus galli	382	195	10.8	1369	1	NPAS_CHICK	NPAS_CHICK mus musculu
310	203.5	11.3	1249	2	Q90Z04	Q90z04 xenopus lae	383	195	10.8	1375	2	Q8ML47	Q8ml47 drosophila
311	203.5	11.3	1316	2	Q7OE16	Q7oe16 anophelae g	384	195	10.8	1375	2	Q94537	Q94537 drosophila
312	203.5	11.3	2052	2	Q8MXU7	Q8mxu7 homo sapien	385	195	10.8	1386	1	ROB3_HUMAN	ROB3_HUMAN mus musculu
313	203.5	11.3	2092	2	Q76KM9	Q76km9 homo sapien	386	195	10.8	1526	2	Q94538	Q94538 drosophila
314	203.5	11.3	2113	2	Q8TD84	Q8td84 homo sapien	387	195	10.8	1526	2	Q9V6D5	Q9v6d5 drosophila
315	203	11.2	483	2	Q7SX76	Q7sx76 brachydantio	388	194.5	10.8	1277	1	CAML_FUGRU	Q98902 fugu tubfip
316	203	11.2	1066	2	Q6ID59	Q6ide9 drosophila	389	194	10.7	949	1	Q9VW27	Q9vw27 drosophila
317	203	11.2	1415	2	Q94155	Q94155 caenorhabdi	390	193.5	10.7	1256	2	NRCA_MOUSE	NRCA_MOUSE mus musculu
318	203	11.2	1415	2	Q80YN8	Q80yn8 mus musculu	391	193	10.7	749	2	Q967D9	Q967d9 drosophila
319	202.5	11.2	496	2	Q7Z075	Q7z075 caenorhabdi	392	193	10.7	775	2	Q6PFS0	Q6pfs0 xenopus lae
320	202.5	11.2	1066	2	Q8MSR5	Q8msr5 drosophila	393	193	10.7	803	2	Q80ZP5	Q80zfs rattus norv
321	202.5	11.2	1946	2	Q68J72	Q68j72 apis mellif	394	193	10.7	902	2	Q81Q17	Q81q17 drosophila
322	202.5	11.2	2828	2	Q9NR99	Q9nr99 homo sapien	395	193	10.7	903	2	Q967D8	Q967d8 drosophila
323	202	11.2	947	1	MUSK_CHICK	Q8axy6 gallus galli	396	193	10.7	903	2	Q9VQY1	Q9vqy1 drosophila

397	193	10.7	949	2	Q8IGN3	O8IGN3	drosophila	470	186	10.3	708	1	KIR2_HUMAN	O6UW16	homo sapien
398	193	10.7	1166	2	Q9QVW4	O9QVW4	rattus sp.	471	186	10.3	899	2	Q7PQM9	O7PQM9	anopheles g
399	193	10.7	1508	2	O6NR34	O6NR34	drosophila	472	186	10.3	1225	2	O6GPE1	O6GPE1	xenopus lae
400	193	10.7	1508	2	O9VOY2	O9VOY2	drosophila	473	186	10.3	2558	2	O6NR91	O6NR91	drosophila
401	193	10.7	1531	2	O967D7	O967D7	drosophila	474	186	10.3	8648	2	O7KOP6	O7KOP6	drosophila
402	193	10.7	2029	1	IAR_DROME	P16621	drosophila	475	185.5	10.3	347	2	O86SN1	O86SN1	homo sapien
403	193	10.7	2029	2	Q9VIS8	O9VIS8	drosophila	476	185.5	10.3	404	1	RAGE_HUMAN	O86SN1	homo sapien
404	192.5	10.7	1150	2	Q8BS24	O8BS24	mus musculus	477	185.5	10.3	702	1	CEAS_HUMAN	O8N4D0	homo sapien
405	192.5	10.7	1209	2	P70232	P70232	mus musculus	478	185.5	10.3	702	2	O8N4D0	O8N4D0	homo sapien
406	192.5	10.7	1259	2	O6PGJ3	O6PGJ3	mus musculus	479	185.5	10.3	3347	2	O8MMJ9	O8MMJ9	bombyx mori
407	192.5	10.7	1260	1	CAML_MOUSE	P16627	mus musculus	480	185.5	10.3	3354	2	O8T101	O8T101	bombyx mori
408	192.5	10.7	1284	1	NRCA_CHICK	P35331	gallus gall	481	185	10.2	582	2	O8RA45	O8RA45	mus musculus
409	192	10.6	399	2	Q8N772	O8N772	homo sapien	482	185	10.2	778	1	KIR3_MOUSE	O8RA45	mus musculus
410	192	10.6	529	2	Q91V87	O91V87	mus musculus	483	185	10.2	789	1	KIR1_RAT	O8RA45	mus musculus
411	192	10.6	602	2	O86YJ9	O86YJ9	homo sapien	484	185	10.2	1020	2	O8NHN0	O8NHN0	homo sapien
412	192	10.6	650	2	O8NA84	O8NA84	homo sapien	485	185	10.2	1294	2	O8W252	O8W252	homo sapien
413	192	10.6	1256	2	O35158	O35158	rattus norv	486	185	10.2	1427	2	O91562	O91562	xenopus lae
414	192	10.6	1304	1	NRCA_HUMAN	O92823	homo sapien	487	184.5	10.2	424	2	O8C6M0	O8C6M0	mus musculus
415	192	10.6	1378	1	ROB2_HUMAN	O9HCX4	homo sapien	488	184.5	10.2	570	2	O6GMZ9	O6GMZ9	xenopus lae
416	191.5	10.6	1060	2	Q9Q2I3	O9Q2I3	rattus norv	489	184.5	10.2	826	2	O7Q1P7	O7Q1P7	anopheles g
417	191	10.6	509	2	Q920C2	O920C2	mus musculus	490	184.5	10.2	3094	2	O695L1	O695L1	homo sapien
418	191	10.6	2154	2	Q8WZ51	O8WZ51	homo sapien	491	184	10.2	421	2	O7PV30	O7PV30	anopheles g
419	190.5	10.5	388	2	O8RA64	O8RA64	mus musculus	492	184	10.2	421	2	O7OLK4	O7OLK4	anopheles g
420	190.5	10.5	1154	2	Q9QVW3	O9QVW3	rattus sp.	493	184	10.2	474	2	O7PKE3	O7PKE3	anopheles g
421	190.5	10.5	1194	2	O6PW35	O6PW35	rattus norv	494	184	10.2	626	1	MAG_RAT	O7PKE3	anopheles g
422	190.5	10.5	1197	2	O6PW38	O6PW38	rattus norv	495	184	10.2	757	1	KIR1_HUMAN	P07722	rattus norv
423	190.5	10.5	1198	2	O6PW37	O6PW37	rattus norv	496	184	10.2	1033	2	O24327	O24327	homo sapien
424	190.5	10.5	1206	2	O6PW36	O6PW36	rattus norv	497	184	10.2	1033	2	O9V643	O9V643	drosophila
425	190.5	10.5	1209	2	O6PW39	O6PW39	rattus norv	498	184	10.2	1302	1	VGR2_BRABE	O8AXJ3	brachydanio
426	190.5	10.5	1214	1	NRCA_RAT	P97666	rattus norv	499	183.5	10.2	2213	2	O7Z5N4	O7Z5N4	homo sapien
427	190.5	10.5	1239	1	ROB3_MOUSE	O6PW34	rattus norv	500	183	10.1	1232	2	O90284	O90284	homo sapien
428	190.5	10.5	1366	1	ROB3_MOUSE	O9Z214	rattus norv	501	183	10.1	1328	2	O21043	O21043	caenorhabdi
429	190.5	10.5	4001	2	O9NL88	O9NL88	drosophila	502	183	10.1	4816	2	O8T103	O8T103	bombyx mori
430	190.5	10.5	4736	2	O9NL88	O9NL88	drosophila	503	182.5	10.1	260	2	O9XXD7	O9XXD7	caenorhabdi
431	190.5	10.5	4796	2	O9W055	O9W055	drosophila	504	182.5	10.1	931	2	O4A087	O4A087	caenorhabdi
432	190	10.5	345	2	O811H7	O811H7	mus musculus	505	182.5	10.1	997	2	O4A087	O4A087	caenorhabdi
433	190	10.5	381	2	O914A4	O914A4	homo sapien	506	182.5	10.1	1083	2	O76698	O76698	caenorhabdi
434	190	10.5	551	2	O8NHN7	O8NHN7	homo sapien	507	182.5	10.1	1098	2	O961D6	O961D6	drosophila
435	190	10.5	619	2	O7PX10	O7PX10	anopheles g	508	182.5	10.1	1332	2	O9BNI17	O9BNI17	drosophila
436	190	10.5	1406	2	O9GPP7	O9GPP7	drosophila	509	182.5	10.1	1332	2	O9VQW7	O9VQW7	drosophila
437	190	10.5	1463	2	O9V008	O9V008	drosophila	510	182.5	10.1	1336	1	VGR1_RAT	P53767	rattus norv
438	189.5	10.5	433	2	O9V644	O9V644	drosophila	511	182.5	10.1	1944	2	O695L3	O695L3	brachydanio
439	189.5	10.5	602	2	O9VFD9	O9VFD9	drosophila	512	182	10.1	626	1	MAG_HUMAN	P20916	homo sapien
440	189.5	10.5	765	2	O9BRQ1	O9BRQ1	aplysia cal	513	182	10.1	877	2	O9GSH3	O9GSH3	halocynthia
441	189.5	10.5	765	2	O9BRQ1	O9BRQ1	aplysia cal	514	182	10.1	2212	2	O8NHN3	O8NHN3	homo sapien
442	189.5	10.5	812	2	O9BK00	O9BK00	aplysia cal	515	182	10.1	17903	2	O7RTL4	O7RTL4	drosophila
443	189.5	10.5	812	2	O9BK00	O9BK00	aplysia cal	516	181.5	10.0	793	2	O70246	O70246	mus musculus
444	189.5	10.5	880	2	O9TWA5	O9TWA5	aplysia cal	517	181.5	10.0	813	2	O8BQC3	O8BQC3	mus musculus
445	189.5	10.5	932	2	O9BKP9	O9BKP9	aplysia cal	518	181.5	10.0	1125	2	O7OEC1	O7OEC1	anopheles g
446	189.5	10.5	932	2	O9TWA6	O9TWA6	aplysia cal	519	181.5	10.0	1197	1	CAML_BRABE	O90478	brachydanio
447	189.5	10.5	1280	2	O909J3	O909J3	gallus gall	520	181.5	10.0	1333	1	VGR1_MOUSE	P35969	mus musculus
448	189	10.5	750	2	O646H5	O646H5	caenorhabdi	521	181	10.0	885	2	O8N237	O8N237	homo sapien
449	188.5	10.4	1032	2	O8AXZ4	O8AXZ4	brachydanio	522	181	10.0	913	2	O8TR35	O8TR35	caenorhabdi
450	188.5	10.4	1036	2	O8SWM3	O8SWM3	drosophila	523	181	10.0	928	2	O19128	O19128	caenorhabdi
451	188.5	10.4	1390	2	O9VNI4	O9VNI4	drosophila	524	181	10.0	955	2	O8MQ86	O8MQ86	caenorhabdi
452	188.5	10.4	1842	2	O81ZY3	O81ZY3	homo sapien	525	181	10.0	1244	2	O69YJ3	O69YJ3	homo sapien
453	188	10.4	529	2	O7TQM3	O7TQM3	rattus norv	526	181	10.0	1263	2	O7Z3B7	O7Z3B7	homo sapien
454	188	10.4	789	1	KIR1_MOUSE	O8W68	mus musculus	527	181	10.0	3198	2	O9U8G8	O9U8G8	manduca sex
455	188	10.4	1177	2	O6GOB1	O6GOB1	xenopus lae	528	181	10.0	5604	2	O8WZ53	O8WZ53	homo sapien
456	187.5	10.4	538	2	O9QY07	O9QY07	mus musculus	529	180.5	10.0	848	2	O25198	O25198	hydra attenu
457	187.5	10.4	1250	2	O88971	O88971	mus musculus	530	180.5	10.0	1242	1	NEPH_MOUSE	O9QZ87	mus musculus
458	187.5	10.4	1259	1	CAML_RAT	O05695	rattus norv	531	180.5	10.0	1256	2	O9Z5S5	O9Z5S5	mus musculus
459	187.5	10.4	1266	1	NGCA_CHICK	O03696	gallus gall	532	180.5	10.0	1256	2	O9ERT59	O9ERT59	mus musculus
460	187.5	10.4	2419	2	O7PXZ1	O7PXZ1	anopheles g	533	180.5	10.0	1256	2	O9J1X1	O9J1X1	mus musculus
461	187	10.4	687	2	O7ZTN4	O7ZTN4	xenopus lae	534	180.5	10.0	1269	2	O6U7I5	O6U7I5	brachydanio
462	187	10.4	778	1	KIR3_HUMAN	O81ZU9	homo sapien	535	180	10.0	413	2	O27418	O27418	manduca sex
463	187	10.4	1470	1	ROB2_MOUSE	O7PQ3	mus musculus	536	180	10.0	609	2	O7QHA0	O7QHA0	anopheles g
464	187	10.4	2133	2	O7PQ39	O7PQ39	anopheles g	537	180	10.0	18412	2	O7Z6E1	O7Z6E1	brachydanio
465	187	10.4	2174	2	O9GQRO	O9GQRO	drosophila	538	179.5	9.9	333	2	O90241	O90241	gallus gall
466	187	10.4	2295	2	O696W0	O696W0	brachydanio	539	179.5	9.9	362	2	O9JH01	O9JH01	rattus norv
467	186.5	10.3	922	2	O904I3	O904I3	brachydanio	540	179.5	9.9	503	2	O9WZ59	O9WZ59	drosophila
468	186.5	10.3	1264	2	O14631	O14631	homo sapien	541	179.5	9.9	804	2	O800Z1	O800Z1	brachydanio
469	186.5	10.3	1889	2	O7Q0X2	O7Q0X2	anopheles g	542	179.5	9.9	806	2	O90Z00	O90Z00	brachydanio

543	179	9.9	300	1	UAMI MOUSE	086792	mus musculus	616	172	9.5	287	2	Q13984	013984	homo sapien
544	179	9.9	300	2	Q8VC39	Q8VC39	mus musculus	617	172	9.5	319	1	A33 MOUSE	091kas	mus musculus
545	179	9.9	626	1	MAG MOUSE	P20191	mus musculus	618	172	9.5	371	2	Q7Q127	07Q127	anopheles g
546	179	9.9	914	2	OBIVU1	OBIVU1	homo sapien	619	172	9.5	1045	2	Q86T37	086T37	homo sapien
547	179	9.9	917	1	ICAS MOUSE	Q60625	mus musculus	620	172	9.5	1320	2	Q96KFE	096KFE	homo sapien
548	179	9.9	1019	2	Q8BTK6	Q8BTK6	mus musculus	621	172	9.5	1320	2	Q86TC9	086TC9	homo sapien
549	178.5	9.9	1234	1	NPHN RAT	Q91044	ratteus norv	622	172	9.5	2403	2	Q8MLD5	08MLD5	anopheles g
550	178.5	9.9	1252	2	Q9JIX2	Q9JIX2	ratteus norv	623	172	9.5	4736	2	Q7Y799	07Y799	mytilus gal
551	178	9.9	310	2	Q7OKJ5	Q7OKJ5	anopheles g	624	172	9.5	7210	2	Q9V7G8	09V7G8	drosophila
552	178	9.9	379	2	Q9CWM1	Q9CWM1	mus musculus	625	171.5	9.5	283	2	Q9VWT6	09VWT6	drosophila
553	178	9.9	413	1	HEMO MANSE	P13398	manduca sex	626	171.5	9.5	307	2	Q94431	094431	ciona intece
554	178	9.9	492	2	Q9ET54	Q9ET54	mus musculus	627	171.5	9.5	1338	2	VGRI HUMAN	09V94	h vasculat
555	178	9.9	853	2	Q6DFX7	Q6DFX7	mus musculus	628	171.5	9.5	2772	2	Q9VAV4	09VAV4	drosophila
556	178	9.9	1073	2	Q9TX18	Q9TX18	caenorhabdi	629	171.5	9.5	2894	2	Q7KRX2	07KRX2	drosophila
557	178	9.9	1081	2	Q69ZT7	Q69ZT7	mus musculus	630	171.5	9.5	26926	2	Q10466	010466	homo sapien
558	177.5	9.8	344	2	Q9VYJ3	Q9VYJ3	drosophila	631	171	9.5	373	2	Q7KYPS	07KYPS	homo sapien
559	177.5	9.8	457	2	Q96OD1	Q96OD1	drosophila	632	171	9.5	464	2	Q16170	016170	homo sapien
560	177.5	9.8	583	1	C166 BOVIN	Q96h13	bos taurus	633	171	9.5	468	2	Q96CAT	096CAT	homo sapien
561	177.5	9.8	717	2	Q7PUQ1	Q7PUQ1	anopheles g	634	171	9.5	526	1	CEAI HUMAN	09V68	homo sapien
562	177.5	9.8	796	2	Q91287	Q91287	pleurodeles	635	171	9.5	534	2	Q86SE4	086SE4	homo sapien
563	177.5	9.8	1249	2	Q7TMZ9	Q7TMZ9	ratteus norv	636	171	9.5	764	2	Q8MQQ1	08MQQ1	drosophila
564	177.5	9.8	1527	2	Q9VZ24	Q9VZ24	drosophila	637	171	9.5	810	2	Q9PS96	09PS96	anopheles g
565	177.5	9.8	1933	2	Q6V3M4	Q6V3M4	mus musculus	638	171	9.5	1255	2	Q7Z3Z9	07Z3Z9	homo sapien
566	177	9.8	376	2	Q90Z71	Q90Z71	brachydantio	639	171	9.5	1257	1	CAML HUMAN	09V10	homo sapien
567	177	9.8	404	2	Q9Y3B9	Q9Y3B9	homo sapien	640	171	9.5	2224	2	Q9ULM1	09ULM1	drosophila
568	177	9.8	577	2	Q80Y42	Q80Y42	mus musculus	641	171	9.5	26926	2	Q8WZB3	08WZB3	homo sapien
569	177	9.8	1331	2	Q7Q623	Q7Q623	anopheles g	642	170.5	9.4	370	2	Q800Y8	0800Y8	brachydantio
570	177	9.8	2242	2	Q9P2P9	Q9P2P9	homo sapien	643	170.5	9.4	501	2	Q6O147	06O147	bos taurus
571	177	9.8	8625	2	Q86CD6	Q86CD6	procambatus	644	170.5	9.4	521	1	C166 RABIT	04651	oryctolagus
572	176.5		350	2	Q6PUN1	Q6PUN1	homo sapien	645	170.5	9.4	540	2	Q8NOZ9	08NOZ9	homo sapien
573	176.5	9.8	510	2	Q7L3B0	Q7L3B0	homo sapien	646	170.5	9.4	591	2	Q6NP04	06NP04	drosophila
574	176.5	9.8	686	1	SILB HUMAN	Q9Y2J6	homo sapien	647	170	9.4	291	2	Q6GJ15	06GJ15	anopheles g
575	176.5	9.8	1106	2	Q8WX93	Q8WX93	homo sapien	648	170	9.4	302	1	Q9JHY1	09JHY1	ratteus norv
576	176.5	9.8	2169	2	Q8AV58	Q8AV58	gallus galli	649	170	9.4	812	1	PGRI XENLA	P23182	anopheles g
577	176.5	9.8	3029	2	Q7Q767	Q7Q767	anopheles g	650	169.5	9.4	265	2	Q7PUT3	07PUT3	anopheles g
578	176.5	9.8	410	2	Q6R3J9	Q6R3J9	bombyx mand	651	169.5	9.4	351	2	Q8VFD3	08VFD3	anopheles g
579	176	9.7	577	2	Q9D281	Q9D281	m mus muscu	652	169.5	9.4	351	2	Q7SY58	07SY58	brachydantio
580	176	9.7	964	2	Q18382	Q18382	caenorhabdi	653	169.5	9.4	402	1	RAGE RAT	06M986	ratteus norv
581	175.5	9.7	1196	2	Q65Z10	Q65Z10	caenorhabdi	654	169.5	9.4	402	2	Q6MG86	06MG86	ratteus norv
582	175.5	9.7	1237	2	Q9B1A2	Q9B1A2	caenorhabdi	655	169.5	9.4	960	2	Q7PV74	07PV74	anopheles g
583	175	9.7	234	2	Q81Z09	Q81Z09	homo sapien	656	169.5	9.4	2200	2	Q7YRF6	07YRF6	canis famli
584	174	9.6	736	2	Q8MY82	Q8MY82	drosophila	657	169	9.4	764	1	TCRR DROME	Q08180	drosophila
585	174	9.6	675	2	Q7T0V5	Q7T0V5	anopheles g	658	169	9.4	814	2	Q9W4U1	09W4U1	drosophila
586	174	9.6	534	2	Q866T2	Q866T2	anopheles g	659	169	9.4	864	2	Q91897	091897	anopheles g
587	174	9.6	210	2	Q7PVL9	Q7PVL9	anopheles g	660	169	9.4	1254	2	Q674V1	0674V1	podocoryne
588	174	9.6	54	2	Q866T2	Q866T2	anopheles g	661	168.5	9.3	800	2	Q86LTP	086LTP	drosophila
589	174	9.6	675	2	Q7T0V5	Q7T0V5	anopheles g	662	168.5	9.3	801	2	Q86LTP	086LTP	drosophila
590	174	9.6	736	2	Q8MY82	Q8MY82	drosophila	663	168.5	9.3	2159	2	Q86PAL2	086PAL2	mus musculus
591	174	9.6	746	2	Q9V930	Q9V930	drosophila	664	168	9.3	215	2	Q9VRL5	09VRL5	drosophila
592	174	9.6	1255	2	Q7YQL7	Q7YQL7	pongo pygma	665	168	9.3	827	2	Q6GN55	06GN55	xenopus lae
593	174	9.6	1255	2	Q7YQL8	Q7YQL8	pan troglod	666	168	9.3	2051	2	Q44338	044338	hirtudo medi
594	174	9.6	1721	2	Q96J10	Q96J10	drosophila	667	167.5	9.3	555	1	C166 CARAU	090304	carassius a
595	174	9.6	2389	2	Q6BE06	Q6BE06	caenorhabdi	668	167.5	9.3	784	2	Q81063	081063	drosophila
596	174	9.6	3375	1	UN52 CABEL	Q06561	caenorhabdi	669	167.5	9.3	939	2	Q9VH85	09VH85	drosophila
597	174	9.6	4650	2	Q15598	Q15598	homo sapien	670	167.5	9.3	1019	1	Q9Y6L9	09Y6L9	homo sapien
598	174	9.6	6658	2	Q76281	Q76281	drosophila	671	167.5	9.3	1694	1	SN MOUSE	062230	mus musculus
599	173.5	9.6	196	2	Q7PUY5	Q7PUY5	anopheles g	672	167.5	9.3	2776	2	Q869A0	0869A0	drosophila
600	173.5	9.6	360	2	Q8MR6	Q8MR6	anopheles g	673	167.5	9.3	2898	2	Q868Z9	0868Z9	drosophila
601	173.5	9.6	442	2	Q6KAT6	Q6KAT6	mus musculus	674	167	9.2	376	2	Q9QW78	09QW78	mus sp. . f
602	173.5	9.6	538	2	Q9NM07	Q9NM07	homo sapien	675	167	9.2	489	2	Q7PGL7	07PGL7	anopheles g
603	173.5	9.6	544	2	Q6UXI8	Q6UXI8	homo sapien	676	167	9.2	551	2	Q8MSN7	08MSN7	drosophila
604	173.5	9.6	600	2	Q7PN36	Q7PN36	anopheles g	677	167	9.2	956	2	Q9W4T9	09W4T9	drosophila
605	173.5	9.6	1021	2	P79757	P79757	gallus galli	678	167	9.2	959	2	Q9N9V9	09N9V9	drosophila
606	173.5	9.6	1235	2	Q7Q0S7	Q7Q0S7	anopheles g	679	167	9.2	1276	2	Q90X22	090X22	brachydantio
607	173.5	9.6	4463	2	Q8MLD8	Q8MLD8	drosophila	680	167	9.2	1356	1	VAR2 HUMAN	P35968	homo sapien
608	173.5	9.6	9270	2	Q8MLD9	Q8MLD9	drosophila	681	167	9.2	2200	1	IAR CABEL	Q9PMn8	caenorhabdi
609	173	9.6	385	2	Q9UQF5	Q9UQF5	homo sapien	682	166.5	9.2	1506	2	Q7Z766	07Z766	brachydantio
610	173	9.6	410	2	Q6R3M0	Q6R3M0	bombyx mori	683	166.5	9.2	4039	2	Q9Z446	09Z446	brachydantio
611	173	9.6	410	2	Q7YZA7	Q7YZA7	bombyx mori	684	166	9.2	576	2	Q8MYR8	08MYR8	drosophila
612	173	9.6	1248	2	Q9XT41	Q9XT41	cercopithe	685	166	9.2	997	2	Q7PXX0	07PXX0	anopheles g
613	172	9.6	357	2	Q8RI12	Q8RI12	mus musculus	686	166	9.2	1232	2	Q8TCG8	08TCG8	homo sapien
614	172.5	9.6	1880	2	Q18465	Q18465	hirtudo medi	687	165.5	9.2	340	2	Q9W3N2	09W3N2	drosophila
615	172.5	9.6	1880	2	Q18465	Q18465	hirtudo medi	688	165.5	9.2	538	2	Q28939	028939	sus acrofa

689	165.5	9.2	646	1	MU18_HUMAN	P43121	homo sapien	762	160.5	8.9	980	1	KFMS_FELCA	P13369	felis silve
690	165.5	9.2	1023	2	Q9UL17	Q9UL17	homo sapien	763	160	8.9	319	1	A33_HUMAN	Q99795	homo sapien
691	165.5	9.2	1193	2	Q9VQW1	Q9VQW1	drosofila	764	160	8.9	485	2	Q801W5	Q801W5	brachydanio
692	165	9.1	584	2	Q9Y3Y8	Q9Y3Y8	homo sapien	765	160	8.9	544	2	Q722Z85	Q722Z85	brachydanio
693	165	9.1	822	1	FGRI_MOUSE	P16092	mus musculu	766	160	8.9	564	1	C166_BRABE	Q90460	brachydanio
694	165	9.1	822	1	FGRI_RAT	O04589	rattus norv	767	160	8.9	564	2	O610X4	O610X4	brachydanio
695	165	9.1	822	2	Q60818	Q60818	mus musculu	768	160	8.9	640	2	Q8BSM2	Q8BSM2	mus musculu
696	165	9.1	998	2	Q9W4Y6	Q9W4Y6	drosofila	769	160	8.9	822	1	FGRI_HUMAN	P13362	homo sapien
697	165	9.1	1014	2	Q8NFA6	Q8NFA6	homo sapien	770	160	8.9	1147	2	O181I0	Q181I0	caenorrhabi
698	165	9.1	2222	2	Q97394	Q97394	drosofila	771	160	8.9	1437	2	O443Z9	Q443Z9	hirudo medi
699	165	9.1	2230	2	Q86B07	Q86B07	drosofila	772	160	8.9	6839	2	Q23550	Q23550	caenorrhabi
700	164.5	9.1	438	2	Q920C3	Q920C3	mus musculu	773	159.5	8.8	570	2	Q8NCE6	Q8NCE6	homo sapien
701	164.5	9.1	583	1	C166_HUMAN	Q13740	homo sapien	774	159.5	8.8	585	2	Q6UY09	Q6UY09	homo sapien
702	164.5	9.1	583	1	C166_RAT	Q35112	rattus norv	775	159.5	8.8	975	2	Q97174	Q97174	drosofila
703	164.5	9.1	639	2	Q96P30	Q96P30	homo sapien	776	159	8.8	226	2	Q7PUJ2	Q7PUJ2	anopheles g
704	164.5	9.1	822	2	O61674	O61674	drosofila	777	159	8.8	816	2	Q91285	Q91285	pleurodeles
705	164.5	9.1	822	2	Q9V6T1	Q9V6T1	drosofila	778	159	8.8	1948	1	PNTS_HUMAN	Q13332	homo sapien
706	164.5	9.1	1247	2	Q700S6	Q700S6	anopheles g	779	158.5	8.8	388	1	BASF_CHICK	P17780	gallus gall
707	164	9.1	310	2	Q68F02	Q68F02	rattus norv	780	158.5	8.8	912	1	ICAE_RABIT	Q28730	oryctolagus
708	164	9.1	310	2	Q9DIM9	Q9DIM9	mus musculu	781	158.5	8.8	1199	2	Q21041	Q21041	caenorrhabi
709	164	9.1	310	2	Q9DB87	Q9DB87	mus musculu	782	158.5	8.8	1215	2	Q7KTI7	Q7KTI7	drosofila
710	164	9.1	310	2	Q9EPK4	Q9EPK4	m junctiona	783	158.5	8.8	1461	2	Q8T9F6	Q8T9F6	drosofila
711	164	9.1	628	1	LU_HUMAN	P50895	homo sapien	784	158.5	8.8	1474	2	Q8T4M0	Q8T4M0	drosofila
712	164	9.1	628	2	Q8FVC7	Q8FVC7	homo sapien	785	158.5	8.8	1503	2	Q7KTI8	Q7KTI8	drosofila
713	164	9.1	812	2	Q8N6T2	Q8N6T2	homo sapien	786	158.5	8.8	1509	2	Q8T9G1	Q8T9G1	drosofila
714	164	9.1	820	2	Q8CIM9	Q8CIM9	mus musculu	787	158.5	8.8	1509	2	Q9VLQ8	Q9VLQ8	anopheles g
715	164	9.1	924	2	Q8TAM9	Q8TAM9	homo sapien	788	158	8.7	242	2	Q7Q1Q0	Q7Q1Q0	anopheles g
716	164	9.1	988	2	Q95R27	Q95R27	drosofila	789	158	8.7	293	2	Q7QC80	Q7QC80	anopheles g
717	164	9.1	1311	2	Q961K8	Q961K8	drosofila	790	158	8.7	360	2	Q61565	Q61565	mus musculu
718	164	9.1	1994	2	Q6ZPE2	Q6ZPE2	mus musculu	791	158	8.7	361	2	Q9CWM7	Q9CWM7	mus sp. - f
719	164	9.1	2176	2	Q6V4S5	Q6V4S5	mus musculu	792	158	8.7	697	2	Q7PMJ7	Q7PMJ7	anopheles g
720	163.5	9.1	483	2	Q9DBP8	Q9DBP8	mus musculu	793	158	8.7	822	2	Q9QVY7	Q9QVY7	rattus sp.
721	163.5	9.1	508	2	Q8CED8	Q8CED8	mus musculu	794	157.5	8.7	346	2	Q9CTL3	Q9CTL3	mus musculu
722	163.5	9.1	508	2	Q8R007	Q8R007	mus musculu	795	157.5	8.7	441	2	Q8CI39	Q8CI39	mus musculu
723	163.5	9.1	513	2	Q6PR64	Q6PR64	mus musculu	796	157.5	8.7	496	2	Q9JIF9	Q9JIF9	mus musculu
724	163.5	9.1	646	2	Q6PR64	Q6PR64	mus musculu	797	157.5	8.7	531	2	Q7OIEY7	Q7OIEY7	anopheles g
725	163.5	9.1	1596	2	Q9HCL6	Q9HCL6	homo sapien	798	157.5	8.7	583	1	C166_MOUSE	Q61480	mus musculu
726	163	9.0	357	2	O18872	Q9HC16	homo sapien	799	157.5	8.7	697	1	SILH_HUMAN	Q961C7	homo sapien
727	163	9.0	924	1	ICAS_HUMAN	Q9UMT0	homo sapien	800	157.5	8.7	939	2	Q967X6	Q967X6	drosofila
728	162.5	9.0	332	2	Q684Q2	Q684Q2	mus musculu	801	157.5	8.7	939	2	Q9VB35	Q9VB35	feline sarc
729	162.5	9.0	353	2	Q68XY3	Q68XY3	homo sapien	802	157.5	8.7	978	1	KFMS_F5VMD	P00545	drosofila
730	162.5	9.0	508	2	Q961A5	Q961A5	homo sapien	803	157.5	8.7	1052	2	Q7PMY4	Q7PMY4	anopheles g
731	162.5	9.0	605	2	Q6GNL9	Q6GNL9	xenopus lae	804	157.5	8.7	1503	2	Q8T4I8	Q8T4I8	drosofila
732	162.5	9.0	628	2	Q9WZ08	Q9WZ08	bos taurus	805	157	8.7	288	1	JAMI_BOVIN	Q9X5E6	bos taurus
733	162.5	9.0	1509	2	Q95P10	Q95P10	drosofila	806	157	8.7	299	1	JAMI_HUMAN	Q9Y6Z4	homo sapien
734	162.5	9.0	1535	2	Q23991	Q23991	drosofila	807	157	8.7	383	2	Q75ML9	Q75ML9	homo sapien
735	162	9.0	773	2	Q7OBL9	Q7OBL9	anopheles g	808	157	8.7	446	2	Q632J6	Q632J6	rattus norv
736	162	9.0	1304	2	Q9VBE5	Q9VBE5	drosofila	809	157	8.7	641	2	Q86SD2	Q86SD2	ciona intes
737	162	9.0	4824	2	Q95YK1	Q95YK1	procambarus	810	157	8.7	734	2	Q961A4	Q961A4	homo sapien
738	161.5	8.9	350	2	Q9VF07	Q9VF07	drosofila	811	157	8.7	742	2	Q96P31	Q96P31	homo sapien
739	161.5	8.9	402	2	Q9NAR0	Q9NAR0	caenorrhabi	812	157	8.7	742	2	Q8N6S2	Q8N6S2	homo sapien
740	161.5	8.9	638	2	Q7O766	Q7O766	anopheles g	813	156.5	8.7	416	1	RAGR_BOVIN	Q8B1B8	mus musculu
741	161.5	8.9	650	2	Q9GKR2	Q9GKR2	bos taurus	814	156.5	8.7	799	2	Q8C3V5	Q8C3V5	bos taurus
742	161.5	8.9	739	2	Q9GKR3	Q9GKR3	bos taurus	815	156.5	8.7	799	2	Q8C1B8	Q8C1B8	mus musculu
743	161.5	8.9	802	2	Q42127	Q42127	xenopus lae	816	156.5	8.7	811	2	Q7QTK5	Q7QTK5	anopheles g
744	161.5	8.9	2335	2	Q9N3X8	Q9N3X8	caenorrhabi	817	156	8.6	525	2	Q9YH43	Q9YH43	mus musculu
745	161.5	8.9	2935	2	Q721Y4	Q721Y4	drosofila	818	156	8.6	692	2	Q800Y9	Q800Y9	brachydanio
746	161.5	8.9	2946	2	Q9W053	Q9W053	drosofila	819	156	8.6	740	2	Q96P29	Q96P29	homo sapien
747	161	8.9	298	2	Q8INK5	Q8INK5	drosofila	820	156	8.6	756	2	Q800Z0	Q800Z0	brachydanio
748	161	8.9	309	2	Q96FL1	Q96FL1	homo sapien	821	156	8.6	977	1	KFMS_MOUSE	P09581	mus musculu
749	161	8.9	310	1	JAM3_HUMAN	Q9BX67	homo sapien	822	156	8.6	978	1	KFMS_RAT	Q00495	rattus norv
750	161	8.9	336	2	Q961T8	Q961T8	drosofila	823	156	8.6	1501	2	Q7KUR9	Q7KUR9	drosofila
751	161	8.9	461	2	Q13854	Q13854	homo sapien	824	156	8.6	1860	2	Q7PQP4	Q7PQP4	anopheles g
752	161	8.9	527	2	Q6ZTR2	Q6ZTR2	homo sapien	825	156	8.6	7158	2	Q23351	Q23351	macaca fasc
753	161	8.9	538	2	Q29123	Q29123	sus scrofa	826	155.5	8.6	761	2	Q95LQ2	Q95LQ2	macaca fasc
754	161	8.9	605	2	Q8TB00	Q8TB00	homo sapien	827	155.5	8.6	880	1	TYO3_MOUSE	P55144	mus musculu
755	161	8.9	693	2	Q8THJ3	Q8THJ3	gallus gall	828	155	8.6	880	2	Q6NZM6	Q6NZM6	mus musculu
756	161	8.9	1327	2	Q8QHD3	Q8QHD3	gallus gall	829	155	8.6	373	2	Q9HEB4	Q9HEB4	homo sapien
757	161	8.9	1345	2	Q8VCD0	Q8VCD0	mus musculu	830	155	8.6	454	2	Q91W54	Q91W54	mus musculu
758	161	8.9	2541	2	Q19663	Q19663	caenorrhabi	831	155	8.6	458	2	Q61351	Q61351	mus musculu
759	160.5	8.9	422	2	Q86CY9	Q86CY9	helicoverpa	832	155	8.6	521	1	CEA1_MOUSE	P31809	mus musculu
760	160.5	8.9	646	2	Q95812	Q95812	homo sapien	833	155	8.6	521	2	Q925P3	Q925P3	mus musculu
761	160.5	8.9	646	2	Q8NHN8	Q8NHN8	homo sapien	834	155	8.6	521	2	Q61352	Q61352	mus musculu

835	155	8.6	707	2	Q7PWJ1	Q7pwj1 anophles g	908	149.5	8.3	360	2	Q8BJ10	Q8bj10 mus musculu
836	155	8.6	819	1	FGRI_CHICK	p21804 gallus gall	909	149.5	8.3	739	1	VCAI_RAT	p29534 rattus norv
837	155	8.6	977	2	Q96RD9	Q96rd9 homo sapien	910	149.5	8.3	815	2	Q805B9	Q805b9 brachydanio
838	155	8.6	1363	1	WGR3_MOUSE	p35917 mus musculu	911	149.5	8.3	1073	2	Q9WI78	Q9wi78 drosophila
839	155	8.6	1367	1	WGR2_MOUSE	p35918 mus musculu	912	149.5	8.3	1250	2	Q8TDY8	Q8tdy8 homo sapien
840	154.5	8.6	602	1	NRGI_CHICK	Q05199 gallus gall	913	149.5	8.3	1501	2	Q9QW00	Q9qw00 rattus norv
841	154.5	8.6	1897	1	PTPF_HUMAN	p10586 homo sapien	914	149.5	8.3	1863	2	Q64605	Q64605 rattus norv
842	154.5	8.6	1898	2	Q86W60	Q86w60 homo sapien	915	149	8.3	335	2	Q75237	Q75237 homo sapien
843	154	8.5	549	2	Q9D006	Q9d006 mus musculu	916	149	8.3	372	2	Q8X1G0	Q8xi10 rattus norv
844	154	8.5	605	2	Q9ES87	Q9es87 mus musculu	917	149	8.3	373	2	Q8R373	Q8r373 mus musculu
845	154	8.5	624	2	Q9ES86	Q9es86 rattus norv	918	149	8.3	388	2	Q9Z151	Q9z151 mus musculu
846	154	8.5	648	2	Q9EPF1	Q9epf1 mus musculu	919	149	8.3	570	2	Q6GLY1	Q6gli1 xenopus lae
847	154	8.5	648	2	Q8R2Y2	Q8r2y2 mus musculu	920	149	8.3	1894	2	Q64487	Q64487 mus musculu
848	154	8.5	686	1	IPL2_HUMAN	Q9p60 h x-linked	921	148.5	8.2	220	2	Q7PXP67	Q7px67 mus musculu
849	154	8.5	816	2	Q86PM4	Q86pm4 hydra acten	922	148.5	8.2	289	2	Q7ZWT0	Q7zwt0 xenopus lae
850	154	8.5	1348	1	WGR2_CONJA	p52583 coturnix co	923	148.5	8.2	476	2	Q7ZXJ8	Q7zxj8 xenopus lae
851	153.5	8.5	280	2	Q93350	Q93350 caenorhabdi	924	148.5	8.2	521	1	C166_CANFA	Q46634 canie famli
852	153.5	8.5	1173	2	Q6NR54	Q6nr54 drosophila	925	148.5	8.2	536	2	Q9GV82	Q9gvr2 drosophila
853	153.5	8.5	2217	2	Q8AV57	Q8av57 gallus gall	926	148.5	8.2	588	1	C166_CHICK	P42232 gallus gall
854	153.5	8.5	6048	2	Q7JN85	Q7jns5 caenorhabdi	927	148.5	8.2	673	2	Q6MZM2	Q6mzm2 homo sapien
855	153	8.5	307	2	Q7PCU3	Q7pcu3 anophles g	928	148.5	8.2	821	2	Q9YH44	Q9yh44 xenopus lae
856	153	8.5	1348	2	Q677M1	Q677m1 gallus gall	929	148.5	8.2	1173	2	Q9VJ78	Q9vj78 drosophila
857	153	8.5	1788	2	Q91AY0	Q9iaj0 xenopus lae	930	148.5	8.2	1501	2	Q7TTI17	Q7tti17 mus musculu
858	152.5	8.4	347	2	PTPD_HUMAN	p23468 homo sapien	931	148.5	8.2	1502	2	Q9QW81	Q9qw81 homo sapien
859	152.5	8.4	509	2	Q6PJ52	Q6pj52 homo sapien	932	148.5	8.2	1887	2	Q9QW67	Q9qw67 mus musculu
860	152.5	8.4	519	1	ECTO_RAT	Q9eqv5 m mman-g pr	933	148.5	8.2	1904	2	Q94K59	Q94k59 mus musculu
861	152.5	8.4	1802	2	Q286J3	Q286j3 cyctocolagus	934	148	8.2	622	2	Q9JKB2	Q9jkb2 mus musculu
862	152.5	8.4	7105	2	Q7PXM3	Q7pxm3 anophles g	935	148	8.2	694	2	Q8SWT7	Q8swt7 drosophila
863	152	8.4	247	2	Q7PVM3	Q7pvm3 anophles g	936	148	8.2	697	2	Q8TC35	Q8tc35 homo sapien
864	152	8.4	636	2	Q22040	Q22040 caenorhabdi	937	147.5	8.2	709	2	Q8IXC7	Q8ixc7 homo sapien
865	152	8.4	687	2	Q9J0J8	Q9j0j8 rattus norv	938	147.5	8.2	229	2	Q7PYL3	Q7pyl3 anophles g
866	152	8.4	783	2	Q86T42	Q86t42 homo sapien	939	147.5	8.2	318	2	Q91664	Q91664 xenopus lae
867	152	8.4	810	2	Q86T41	Q86t41 anophles g	940	147.5	8.2	331	2	Q63239	Q63239 rattus norv
868	152	8.4	880	1	TIO3_RAT	p55146 rattus norv	941	147.5	8.2	403	1	PAGE_MOUSE	Q62151 mus musculu
869	152	8.4	1024	2	Q63H20	Q63hj3 homo sapien	942	147.5	8.2	446	2	Q63237	Q63237 rattus norv
870	152	8.4	1092	2	Q91ZT0	Q91zt0 rattus norv	943	147.5	8.2	573	2	Q6GNS0	Q6gns0 xenopus lae
871	152	8.4	1141	1	MYPS_HUMAN	Q00872 homo sapien	944	147.5	8.2	876	2	Q78B87	Q78b87 mus musculu
872	152	8.4	1148	2	Q8N3T2	Q8n3t2 homo sapien	945	147.5	8.2	1499	2	Q90815	Q90815 gallus gall
873	152	8.4	1148	2	Q8N3R4	Q8n3r4 homo sapien	946	147	8.1	402	2	Q35444	Q35444 mus musculu
874	152	8.4	1148	2	Q8N3R4	Q8n3r4 homo sapien	947	147	8.1	549	2	Q9NOS3	Q9nos3 homo sapien
875	152	8.4	1148	2	Q86T39	Q86t39 homo sapien	948	147	8.1	739	1	PECI_BOVIN	p51866 bos taurus
876	152	8.4	1171	2	Q86T38	Q86t38 homo sapien	949	147	8.1	1044	2	Q96IW3	Q96i13 homo sapien
877	152	8.4	1171	2	Q86T38	Q86t38 homo sapien	950	147	8.1	1237	2	Q75147	Q75147 homo sapien
878	152	8.4	1343	1	WGR2_RAT	Q08775 rattus norv	951	147	8.1	1252	2	Q9JL11	Q9jl11 mus musculu
879	152	8.4	1363	2	Q91ZT1	Q91ztl rattus norv	952	146.5	8.1	275	2	Q7PVM4	Q7pvm4 anophles g
880	151.5	8.4	229	2	Q7PVK5	Q7pvk5 anophles g	953	146.5	8.1	291	2	Q6S807	Q6s807 homo sapien
881	151.5	8.4	229	2	Q7PUC4	Q7puc4 anophles g	954	146.5	8.1	326	2	Q8NCT7	Q8nc17 homo sapien
882	151.5	8.4	344	1	CEA6_HUMAN	p40199 homo sapien	955	146.5	8.1	468	2	Q9XV08	Q9xy08 bombyx mori
883	151.5	8.4	344	2	Q13774	Q13774 homo sapien	956	146.5	8.1	484	2	Q99J08	Q99j08 mus musculu
884	151.5	8.4	564	2	Q7ZU00	Q7zu00 brachydanio	957	146.5	8.1	606	2	Q9E8S8	Q9e8s8 rattus norv
885	151.5	8.4	847	2	Q8BPR2	Q8bpr2 m mus muscu	958	146.5	8.1	648	2	Q9BPP2	Q9bpf2 rattus norv
886	151.5	8.4	847	2	Q8C4T3	Q8c4t3 mus musculu	959	146.5	8.1	773	2	Q9NSW7	Q9nsw7 homo sapien
887	151.5	8.4	948	2	Q9TID7	Q9tid7 trichosurus	960	146.5	8.1	847	2	Q8N475	Q8n475 homo sapien
888	151.5	8.4	1898	2	Q9EQ17	Q9eq17 mus musculu	961	146.5	8.1	850	2	Q9ULF7	Q9ulf7 homo sapien
889	151	8.4	1156	2	Q699P0	Q699p0 antheraea p	962	146.5	8.1	1280	2	Q9BPP2	Q9bpf2 mus musculu
890	151	8.4	413	2	Q676C3	Q676c3 ciklopleura	963	146	8.1	309	2	Q7QFT7	Q7qft7 anophles g
891	150.5	8.3	422	2	Q7RTV9	Q7rtv9 homo sapien	964	146	8.1	486	2	Q8CGH8	Q8cgh8 mus musculu
892	150.5	8.3	437	2	Q8NPS6	Q8nps6 homo sapien	965	146	8.1	549	2	Q9JIB9	Q9jib9 mus musculu
893	150.5	8.3	509	2	Q91YK7	Q91yk7 mus musculu	966	146	8.1	738	2	F79390	p79390 bos primige
894	150.5	8.3	510	2	Q96K15	Q96k15 homo sapien	967	146	8.1	782	2	Q61563	Q61563 mus musculu
895	150.5	8.3	510	2	Q96NY8	Q96ny8 homo sapien	968	146	8.1	790	2	Q8C4N3	Q8c4n3 mus musculu
896	150.5	8.3	824	2	Q90749	Q90749 gallus gall	969	146	8.1	827	1	TRKC_CHICK	Q91044 gallus gall
897	150.5	8.3	888	2	Q7ZMW9	Q7zwm9 xenopus lae	970	146	8.1	1087	2	Q7ZY71	Q7zy71 xenopus lae
898	150.5	8.3	961	1	ROB4_RAT	Q80w87 rattus norv	971	146	8.1	1088	1	PGDS_RAT	p20786 rattus norv
899	150.5	8.3	1298	1	WGR3_HUMAN	p35916 homo sapien	972	146	8.1	1089	1	FGDS_MOUSE	p26618 mus musculu
900	150.5	8.3	1298	1	Q86W08	Q86w08 homo sapien	973	146	8.1	1089	2	Q7TSJ3	Q7tsj3 mus musculu
901	150.5	8.3	1363	2	Q86W07	Q86w07 homo sapien	974	145.5	8.1	292	2	Q66172	Q66172 brachydanio
902	150	8.3	343	2	Q7TP22	Q7tp22 rattus norv	975	145.5	8.1	504	2	Q6NNA1	Q6nn12 drosophila
903	150	8.3	686	1	IPL2_MOUSE	Q9eif6 mus musculu	976	145.5	8.1	508	2	Q9VGD2	Q9vgd2 drosophila
904	150	8.3	711	2	Q24Z05	Q24z05 drosophila	977	145.5	8.1	520	2	Q9Z5P2	Q9z5p2 mus musculu
905	150	8.3	977	2	Q6NXV8	Q6nxv8 mus musculu	978	145.5	8.1	664	2	Q9VGD3	Q9vgd3 drosophila
906	150	8.3	1171	2	Q86T48	Q86t48 homo sapien	979	145.5	8.1	739	1	VCAI_MOUSE	p29533 mus musculu
907	149.5	8.3	349	1	CEA6_HUMAN	p31997 homo sapien	980	145.5	8.1	739	2	Q91X98	Q91x98 mus musculu

981	145.5	8.1	808	1	FGR4_MOUSE	Q03142	mus musculus	1054	141	7.8	821	1	FGR2_HUMAN	P21802	homo sapien
982	145.5	8.1	831	2	Q71S79	Q71S79	gallus gall	1055	141	7.8	879	2	Q8V199	Q8V199	rattus norv
983	145.5	8.1	1012	1	ROB4_MOUSE	Q8C310	mus musculus	1056	141	7.8	888	2	Q8V1A0	Q8V1A0	rattus norv
984	145.5	8.1	1898	2	Q64604	Q64604	x proteine-t	1057	141	7.8	977	2	Q98S01	Q98S01	danio nigro
985	145	8.0	259	2	Q9V5B2	Q9V5B2	homo sapien	1058	140.5	7.8	705	2	Q63710	Q63710	rattus rat
986	145	8.0	373	2	Q920S5	Q920S5	mus musculus	1059	140.5	7.8	737	2	Q965M3	Q965M3	caenorhabdi
987	145	8.0	622	2	Q9ES5S	Q9ES5S	mus musculus	1060	140.5	7.8	743	2	Q6P4H5	Q6P4H5	homo sapien
988	145	8.0	782	2	Q9ETZ3	Q9ETZ3	oryctolagus	1061	140.5	7.8	790	2	Q906J9	Q906J9	gallus gall
989	145	8.0	812	2	Q8M257	Q8M257	caenorhabdi	1062	140.5	7.8	823	1	CEK3_CHICK	P18461	gallus gall
990	145	8.0	878	2	Q8GV22	Q8GV22	mytilus gal	1063	140.5	7.8	1079	2	Q6E7G6	P16234	canis famil
991	145	8.0	972	1	KFMS_HUMAN	P07333	homo sapien	1064	140.5	7.8	1089	1	PGDS_HUMAN	Q91A99	homo sapien
992	145	8.0	972	2	Q86VW7	Q86VW7	homo sapien	1065	140.5	7.8	2164	2	Q91A99	Q91A99	gallus gall
993	145	8.0	1450	2	Q7QCP2	Q7QCP2	anopheles g	1066	140	7.8	562	2	Q6VNR7	Q6VNR7	brachydanio
994	144.5	8.0	203	2	Q7PVM1	Q7PVM1	anopheles g	1067	140	7.8	622	2	Q9R0J6	Q9R0J6	mus musculus
995	144.5	8.0	421	2	Q9NBB2	Q9NBB2	drosophila	1068	140	7.8	650	2	Q99XK6	Q99XK6	mus musculus
996	144.5	8.0	606	2	Q6IRH8	Q6IRH8	rattus norv	1069	140	7.8	738	2	Q7QYK6	Q7QYK6	anopheles g
997	144.5	8.0	739	2	Q8K0X1	Q8K0X1	mus musculus	1070	140	7.8	752	2	Q9XY84	Q9XY84	hydra atten
998	144.5	8.0	754	2	Q8BZ76	Q8BZ76	m mus mescu	1071	140	7.8	800	2	Q990S2	Q990S2	mus musculus
999	144.5	8.0	880	2	Q8QFP9	Q8QFP9	anopheles lae	1072	140	7.8	800	2	Q7TSI8	Q7TSI8	mus musculus
1000	144	8.0	260	2	Q7P2J3	Q7P2J3	anopheles g	1073	140	7.8	800	2	Q918X3	Q918X3	brachydanio
1001	144	8.0	278	2	Q9QYL3	Q9QYL3	mus musculus	1074	140	7.8	801	1	FGR3_MOUSE	Q61851	mus musculus
1002	144	8.0	413	2	Q6ZN11	Q6ZN11	homo sapien	1075	140	7.8	879	1	FPRP_HUMAN	Q9P2B2	homo sapien
1003	144	8.0	422	2	Q8WR61	Q8WR61	lymantia d	1076	140	7.8	890	1	TYO3_HUMAN	Q66418	homo sapien
1004	144	8.0	434	2	Q6DN72	Q6DN72	homo sapien	1077	140	7.8	890	2	Q86VY3	Q86VY3	homo sapien
1005	144	8.0	438	2	Q9JLB7	Q9JLB7	mus musculus	1078	140	7.8	972	2	Q99662	Q99662	homo sapien
1006	144	8.0	510	2	Q9JLB8	Q9JLB8	mus musculus	1079	140	7.8	976	1	KIT_HUMAN	P10721	homo sapien
1007	144	8.0	542	2	Q8NHN5	Q8NHN5	homo sapien	1080	140	7.8	966	2	Q6IQ28	Q6IQ28	homo sapien
1008	144	8.0	891	2	Q25177	Q25177	hydra atten	1081	140	7.8	1097	2	Q7QCP0	Q7QCP0	anopheles g
1009	143.5	7.9	296	2	Q640C0	Q640C0	anopheles lae	1082	140	7.8	2888	2	Q8MMK1	Q8MMK1	bombyx mori
1010	143.5	7.9	300	2	Q7SVY0	Q7SVY0	anopheles lae	1083	140	7.8	3239	2	Q8T102	Q8T102	bombyx mori
1011	143.5	7.9	430	2	Q8N4F1	Q8N4F1	homo sapien	1084	140	7.8	4203	2	Q965G2	Q965G2	caenorhabdi
1012	143.5	7.9	1177	2	Q21391	Q21391	caenorhabdi	1085	140	7.8	4219	2	Q9NL87	Q9NL87	caenorhabdi
1013	143.5	7.9	12268	2	Q8MQ08	Q8MQ08	caenorhabdi	1086	140	7.8	4369	2	Q8MXD7	Q8MXD7	caenorhabdi
1014	143.5	7.9	13100	2	Q09165	Q09165	caenorhabdi	1087	140	7.8	4447	2	Q8MXD8	Q8MXD8	caenorhabdi
1015	143	7.9	442	2	Q8C306	Q8C306	mus musculus	1088	140	7.8	4488	2	Q9TXK2	Q9TXK2	caenorhabdi
1016	143	7.9	630	1	SMP_COTLA	Q92154	coturnix co	1089	139.5	7.7	419	1	PSG1_HUMAN	P11464	homo sapien
1017	143	7.9	688	2	Q55035	Q55035	mus musculus	1090	139.5	7.7	422	2	Q96B03	Q96B03	homo sapien
1018	143	7.9	688	2	Q8K1H4	Q8K1H4	mus musculus	1091	139.5	7.7	515	2	Q96F05	Q96F05	homo sapien
1019	143	7.9	814	2	Q9VNP2	Q9VNP2	drosophila	1092	139.5	7.7	544	2	Q7Z9Y7	Q7Z9Y7	anopheles lae
1020	143	7.9	972	2	Q76110	Q76110	callithrix	1093	139.5	7.7	670	2	Q7Z247	Q7Z247	brachydanio
1021	143	7.9	977	2	Q918N6	Q918N6	brachydanio	1094	139.5	7.7	739	2	Q28260	Q28260	canis famil
1022	143	7.9	1011	2	Q24273	Q24273	drosophila	1095	139.5	7.7	743	2	Q6P1M7	Q6P1M7	homo sapien
1023	143	7.9	1383	2	Q70840	Q70840	anopheles g	1096	139.5	7.7	821	1	FGR2_MOUSE	P21803	mus musculus
1024	142.5	7.9	334	2	Q8NBY8	Q8NBY8	homo sapien	1097	139.5	7.7	1052	1	FGR2_MOUSE	Q09147	drosophila
1025	142.5	7.9	336	2	Q9UPK8	Q9UPK8	homo sapien	1098	139.5	7.7	1200	2	Q676A1	Q676A1	oikopleura
1026	142.5	7.9	435	1	PSG6_HUMAN	Q00889	homo sapien	1099	139	7.7	403	2	Q6NZV3	Q6NZV3	brachydanio
1027	142.5	7.9	515	2	Q96RE0	Q96RE0	homo sapien	1100	139	7.7	416	2	Q96360	Q96360	hyphantria
1028	142.5	7.9	739	1	VCAL_HUMAN	Q9NKA6	homo sapien	1101	139	7.7	763	2	Q95YM9	Q95YM9	halocynthia
1029	142.5	7.9	739	1	VCAL_HUMAN	P19320	homo sapien	1102	139	7.7	824	2	Q91286	Q91286	pleurodeles
1030	142.5	7.9	956	2	UNSD_MOUSE	Q8K1E2	mus musculus	1103	139	7.7	976	2	Q9W755	Q9W755	brachydanio
1031	142.5	7.9	1019	2	Q8UVR8	Q8UVR8	fugu rubrip	1104	138.5	7.7	313	2	Q8UW13	Q8UW13	lapemis har
1032	142.5	7.9	1052	2	Q9VUC8	Q9VUC8	drosophila	1105	138.5	7.7	360	2	Q8N732	Q8N732	homo sapien
1033	142.5	7.9	1344	2	Q8WR42	Q8WR42	caenorhabdi	1106	138.5	7.7	377	2	Q9V0Y0	Q9V0Y0	drosophila
1034	142	7.9	345	2	Q8MPV0	Q8MPV0	caenorhabdi	1107	138.5	7.7	413	2	Q26438	Q26438	hyalophora
1035	142	7.9	494	2	Q9ESC6	Q9ESC6	mus musculus	1108	138.5	7.7	419	2	Q96QJ5	Q96QJ5	homo sapien
1036	142	7.9	505	2	Q9U965	Q9U965	geodia cydo	1109	138.5	7.7	719	2	Q9U4G1	Q9U4G1	drosophila
1037	142	7.9	806	1	CEK2_CHICK	P18460	gallus gall	1110	138.5	7.7	1896	2	Q91J61	Q91J61	geodia cydo
1038	142	7.9	1252	2	Q9EO59	Q9EO59	mus musculus	1111	138	7.6	313	2	Q9U964	Q9U964	geodia cydo
1039	142	7.9	1253	2	Q9EO58	Q9EO58	mus musculus	1112	138	7.6	515	1	PVRI_PIG	Q9J176	sus scrofa
1040	141.5	7.8	334	2	Q9UPK9	Q9UPK9	homo sapien	1113	138	7.6	767	2	Q86VY7	Q86VY7	homo sapien
1041	141.5	7.8	333	2	Q75238	Q75238	homo sapien	1114	138	7.6	1087	1	PGDS_XENTLA	P26619	anopheles lae
1042	141.5	7.8	881	1	Q965W2	Q965W2	caenorhabdi	1115	137.5	7.6	357	2	Q63338	Q63338	rattus norv
1043	141.5	7.8	953	1	UNSD_HUMAN	Q6UX24	homo sapien	1116	137.5	7.6	385	2	Q9VXK8	Q9VXK8	drosophila
1044	141.5	7.8	1007	1	ROB4_HUMAN	Q8W275	homo sapien	1117	137.5	7.6	413	1	HEMO_HYACE	P25033	hyalophora
1045	141.5	7.8	1227	2	Q21038	Q21038	caenorhabdi	1118	137.5	7.6	419	1	PSG4_HUMAN	Q00088	homo sapien
1046	141.5	7.8	1447	2	Q16779	Q16779	caenorhabdi	1119	137.5	7.6	428	2	Q9BRW2	Q9BRW2	homo sapien
1047	141.5	7.8	2000	2	Q97791	Q97791	oryctolagus	1120	137.5	7.6	463	2	Q66U72	Q66U72	anopheles lae
1048	141	7.8	276	2	Q6P0R7	Q6P0R7	brachydanio	1121	137.5	7.6	740	1	PECT_PIG	Q95242	sus scrofa
1049	141	7.8	338	2	Q6DHD4	Q6DHD4	brachydanio	1122	137.5	7.6	977	2	Q985U4	Q985U4	danio albol
1050	141	7.8	432	2	Q6DDE7	Q6DDE7	anopheles lae	1123	137.5	7.6	1040	2	Q8NHN2	Q8NHN2	homo sapien
1051	141	7.8	456	2	Q7PUM9	Q7PUM9	anopheles g	1124	137.5	7.6	1379	2	P79701	P79701	coturnix co
1052	141	7.8	636	2	Q6DCI3	Q6DCI3	anopheles lae	1125	137	7.6	366	2	Q6NVZ3	Q6NVZ3	homo sapien
1053	141	7.8	815	2	Q8AYP3	Q8AYP3	brachydanio	1126	137	7.6	420	2	Q68DM9	Q68DM9	homo sapien

1127	137	7.6	424	1	PSGA_HUMAN	Q15235 homo sapien	1200	133.5	7.4	888	1	UFO_MOUSE	Q00993 mus musculus
1128	137	7.6	448	2	O8JGL7	O8JGL7 ratius norv	1201	133.5	7.4	888	2	O8UYO3	Q80943 mus musculus
1129	137	7.6	448	2	O8JHL7	O8JHL7 ratius norv	1202	133.5	7.4	959	2	O8UYA9	Q69uq3 ambystoma m
1130	137	7.6	459	2	O63093	O63093 ratius norv	1203	133.5	7.4	1598	2	O9P214	Q9P214 homo sapien
1131	137	7.6	459	2	O8JHL6	O8JHL6 ratius norv	1204	133	7.4	317	2	O9ESA3	Q9ESA3 ratius norv
1132	137	7.6	517	1	PVR1_HUMAN	Q15223 homo sapien	1205	133	7.4	323	2	O9ESA2	Q9ESA2 ratius norv
1133	137	7.6	662	2	O8MOZ9	O8MOZ9 drosophila	1206	133	7.4	366	2	O9N680	Q9N680 drosophila
1134	137	7.6	662	2	O9VGDO	O9VGDO drosophila	1207	133	7.4	383	2	O18431	O18431 geodia cydo
1135	137	7.6	778	1	TRKA_CHICK	O91009 gallus galli	1208	133	7.4	541	2	O95XJ7	Q95XJ7 caenorhabdi
1136	137	7.6	977	2	O9ESD2	O9ESD2 danio kerri	1209	133	7.4	612	2	O95CX4	Q95CX4 homo sapien
1137	136.5	7.6	345	2	Q7PVU1	Q7PVU1 anopheles g	1210	133	7.4	802	1	PER4_HUMAN	PER4_HUMAN
1138	136.5	7.6	459	2	O8EX91	O8EX91 homo sapien	1211	133	7.4	802	2	O8TDK0	Q8TDK0 homo sapien
1139	136.5	7.6	498	2	O9UBP9	Q9UBP9 homo sapien	1212	133	7.4	807	2	O6DD66	Q6DD66 xenopus lae
1140	136.5	7.6	677	2	O8QHL2	O8QHL2 gallus galli	1213	133	7.4	818	2	O91742	Q91742 xenopus lae
1141	136.5	7.6	738	1	PECL_HUMAN	P16284 homo sapien	1214	133	7.4	818	2	O9PSV9	Q9PSV9 xenopus lae
1142	136.5	7.6	3100	2	O7KYN5	O7KYN5 homo sapien	1215	133	7.4	839	1	TRKC_HUMAN	O16288 homo sapien
1143	136	7.5	229	2	Q7Q9S4	Q7Q9S4 anopheles g	1216	133	7.4	839	2	O756E2	O756E2 homo sapien
1144	136	7.5	298	2	O8C5K9	O8C5K9 mus musculu	1217	133	7.4	974	2	O98SU3	Q98SU3 danio dangi
1145	136	7.5	298	2	O8CE95	O8CE95 mus musculu	1218	133	7.4	1091	2	O9YH41	Q9YH41 gallus galli
1146	136	7.5	298	2	O9J159	O9J159 m vasculat	1219	132.5	7.3	393	2	P97547	P97547 ratius norv
1147	136	7.5	393	2	O95727	O95727 homo sapien	1220	132.5	7.3	411	2	O15228	O15228 homo sapien
1148	136	7.5	903	2	O8N9C0	O8N9C0 homo sapien	1221	132.5	7.3	419	2	O68CR6	O68CR6 homo sapien
1149	136	7.5	976	2	O8UFR5	O8UFR5 brachydantio	1222	132.5	7.3	419	2	O6P520	Q6P520 homo sapien
1150	135.5	7.5	232	2	Q7PJ16	Q7PJ16 anopheles g	1223	132.5	7.3	423	2	O8BU57	O8BU57 homo sapien
1151	135.5	7.5	326	2	O9N166	O9N166 papio hamad	1224	132.5	7.3	426	1	PSGB_HUMAN	PSGB_HUMAN
1152	135.5	7.5	442	2	O7PT04	O7PT04 anopheles g	1225	132.5	7.3	492	2	O7QD44	Q7QD44 homo sapien
1153	135.5	7.5	762	2	O7ITW8	O7ITW8 homo sapien	1226	132.5	7.3	533	2	O8NCB6	O8NCB6 homo sapien
1154	135.5	7.5	822	2	O91288	O91288 pleurodeles	1227	132.5	7.3	534	2	O8NB18	O8NB18 homo sapien
1155	135.5	7.5	975	2	P79750	P79750 figu rubrip	1228	132.5	7.3	584	2	O90989	Q90989 gallus galli
1156	135.5	7.5	13133	2	O71A42	O71A42 caenorhabdi	1229	132.5	7.3	620	2	O61GJ3	O61GJ3 drosophila
1157	135	7.5	332	2	O640J3	O640J3 xenopus tro	1230	132.5	7.3	626	2	O90880	Q90880 gallus galli
1158	135	7.5	393	2	O61RX2	O61RX2 homo sapien	1231	132.5	7.3	671	2	O63711	Q63711 ratius ratt
1159	135	7.5	464	2	O6GL25	O6GL25 xenopus tro	1232	132.5	7.3	800	2	O9JHX9	O9JHX9 ratius norv
1160	135	7.5	802	2	O95M13	O95M13 bos taurus	1233	132.5	7.3	856	2	O62121	Q62121 mus musculu
1161	135	7.5	817	2	O8UJ38	O8UJ38 brachydantio	1234	132.5	7.3	1087	2	O9PUP6	Q9PUP6 gallus galli
1162	134.5	7.4	242	2	O46604	O46604 sus scrofa	1235	132	7.3	201	2	O7PX42	O7PX42 anopheles g
1163	134.5	7.4	263	2	Q7TPW5	Q7TPW5 mus musculu	1236	132	7.3	387	2	O86XK7	Q86XK7 homo sapien
1164	134.5	7.4	348	2	O8NFM3	O8NFM3 homo sapien	1237	132	7.3	408	2	O8KO94	Q8KO94 m hypobdecti
1165	134.5	7.4	419	1	PSG7_HUMAN	O13046 homo sapien	1238	132	7.3	412	2	O6MZ54	O6MZ54 homo sapien
1166	134.5	7.4	426	2	O64HX5	O64HX5 oncorhynch	1239	132	7.3	502	2	O9Z200	Q9Z200 mus musculu
1167	134.5	7.4	480	2	PSG3_HUMAN	Q16557 homo sapien	1240	132	7.3	582	2	O95N25	Q95N25 bos taurus
1168	134.5	7.4	480	2	Q9PSD1	Q9PSD1 xenopus . fi	1241	132	7.3	992	2	O8AXU0	Q8AXU0 oncorhynch
1169	134.5	7.4	493	2	O6P5Y4	O6P5Y4 homo sapien	1242	132	7.3	1048	2	P79749	P79749 figu rubrip
1170	134.5	7.4	659	2	O659F2	O659F2 homo sapien	1243	131.5	7.3	298	1	JAM2_HUMAN	JAM2_HUMAN
1171	134.5	7.4	659	2	O6ZNM1	O6ZNM1 homo sapien	1244	131.5	7.3	298	2	O6YNC1	O6YNC1 homo sapien
1172	134.5	7.4	660	2	Q7Z6B1	Q7Z6B1 homo sapien	1245	131.5	7.3	312	2	O6UXG6	Q6UXG6 homo sapien
1173	134.5	7.4	782	2	O8OTU8	O8OTU8 mus musculu	1246	131.5	7.3	370	2	O6MZQ3	Q6MZQ3 homo sapien
1174	134.5	7.4	1205	2	O8BU70	O8BU70 mus musculu	1247	131.5	7.3	480	2	O9PSC9	Q9PSC9 xenopus . fi
1175	134.5	7.4	1235	2	O95428	O95428 homo sapien	1248	131.5	7.3	739	2	O865F2	O865F2 oryctolagus
1176	134.5	7.4	19066	2	O801W8	O801W8 brachydantio	1249	131.5	7.3	814	2	O6GNP8	O6GNP8 xenopus lae
1177	134	7.4	217	2	O6KGN0	O6KGN0 bacterioph	1250	131	7.3	259	2	O8WR47	O8WR47 caenorhabdi
1178	134	7.4	238	2	Q20339	Q20339 caenorhabdi	1251	131	7.3	298	2	O9GL74	Q9GL74 cercopithec
1179	134	7.4	283	2	O9VNR0	O9VNR0 drosophila	1252	131	7.3	327	2	O96107	Q96107 homo sapien
1180	134	7.4	294	2	O6KGN1	O6KGN1 bacterioph	1253	131	7.3	330	2	O63241	O63241 ratius norv
1181	134	7.4	321	2	O9DEB6	O9DEB6 gallus galli	1254	131	7.3	342	2	O9ESB1	Q9ESB1 ratius norv
1182	134	7.4	397	2	O6XRC3	O6XRC3 homo sapien	1255	131	7.3	355	2	O7OLW7	Q7OLW7 anopheles g
1183	134	7.4	486	2	O9DER4	O9DER4 gallus galli	1256	131	7.3	408	2	O91WP1	Q91WP1 mus musculu
1184	134	7.4	533	2	O9DER5	O9DER5 gallus galli	1257	131	7.3	408	2	O8BVF6	O8BVF6 mus musculu
1185	134	7.4	612	2	Q9Z2P9	Q9Z2P9 mus musculu	1258	131	7.3	429	2	O6VAN7	O6VAN7 bos taurus
1186	134	7.4	825	2	O6VNS1	O6VNS1 mus musculu	1259	131	7.3	782	2	O9ESB5	Q9ESB5 ratius norv
1187	134	7.4	864	1	TRKC_RAT	O03351 ratius norv	1260	131	7.3	935	2	O640T5	O640T5 xenopus tro
1188	134	7.4	1147	1	KULS_RABBIT	P92924 oryctolagus	1261	131	7.3	978	2	O9XSR3	O9XSR3 canis famli
1189	134	7.4	283	2	O7QGF4	O7QGF4 anopheles g	1262	131	7.3	1097	1	PGDR_RAT	PGDR_RAT
1190	133.5	7.4	289	2	O9QY15	O9QY15 mus musculu	1263	131	7.3	1106	1	PGDR_HUMAN	PGDR_HUMAN
1191	133.5	7.4	332	2	O6P359	O6P359 xenopus tro	1264	130.5	7.2	295	2	O9GL75	Q9GL75 bos taurus
1192	133.5	7.4	335	1	PSG2_HUMAN	P11465 homo sapien	1265	130.5	7.2	295	2	O9QYL6	Q9QYL6 mus musculu
1193	133.5	7.4	374	2	Q7QB08	Q7QB08 anopheles g	1266	130.5	7.2	295	2	O9Z2H8	Q9Z2H8 mus musculu
1194	133.5	7.4	584	2	O98921	O98921 gallus galli	1267	130.5	7.2	310	1	FCGB_HUMAN	P11994 homo sapien
1195	133.5	7.4	597	1	STLL_PANTR	O95110 pan troglod	1268	130.5	7.2	323	1	FCGC_HUMAN	P11995 h basiglin p
1196	133.5	7.4	626	2	O98922	O98922 gallus galli	1269	130.5	7.2	385	1	BASI_HUMAN	P25613 h basiglin p
1197	133.5	7.4	729	1	FGRI_DROME	O07407 drosophila	1270	130.5	7.2	523	2	O80ZE2	Q80ZE2 mus musculu
1198	133.5	7.4	755	2	O8CCF8	O8CCF8 mus musculu	1271	130.5	7.2	569	1	SILP_MOUSE	Q920G3 mus musculu
1199	133.5	7.4	879	2	O6PE80	O6PE80 mus musculu	1272	130.5	7.2	707	2	O9TT07	Q9TT07 canis famli

1273	130.5	7.2	775	2	097754	097754	oryctolagus	1346	126.5	7.0	722	2	06GNB3	06gnb3	xenopus lae
1274	130.5	7.2	873	2	098949	098949	gallus gall	1347	126.5	7.0	723	2	086Y14	086y14	homo sapien
1275	130	7.2	325	2	095791	095791	homo sapien	1348	126.5	7.0	723	2	077589	077589	equus caball
1276	130	7.2	332	1	CD22_PANPA	09n16	pan paniscus	1349	126.5	7.0	1099	2	077WR8	077wr8	mus musculus
1277	130	7.2	332	1	CD22_PANTR	09n16	pan troglod	1350	126.5	7.0	1212	2	095YGO	095ygo	drosoophila
1278	130	7.2	334	2	0925F2	0925F2	mus musculus	1351	126	7.0	168	2	08MT25	08mt25	ovis aries
1279	130	7.2	637	2	0922E0	0922E0	mus musculus	1352	126	7.0	204	2	063ZH7	063zh7	xenopus lae
1280	130	7.2	727	1	PECI_MOUSE	0922E0	mus musculus	1353	126	7.0	553	2	08WXJ5	08wxj5	homo sapien
1281	130	7.2	732	2	08CAM4	08CAM4	mus musculus	1354	126	7.0	822	1	TRXB_HUMAN	016620	homo sapien
1282	129.5	7.2	208	2	0866F1	0866F1	pongo pygma	1355	126	6.9	828	2	09D6K3	09d6k3	xenopus lae
1283	129.5	7.2	272	2	07OI02	07OI02	anopheles g	1356	125	6.9	831	2	08WXJ7	08wxj7	homo sapien
1284	129.5	7.2	346	2	P92027	P92027	anopheles g	1357	125.5	6.9	251	2	009970	009970	caenorhabdi
1285	129.5	7.2	365	2	06VANS	06VANS	bos taurus	1358	125.5	6.9	278	2	061350	061350	mus musculus
1286	129.5	7.2	372	2	06VAN6	06VAN6	bos taurus	1359	125.5	6.9	341	2	061353	061353	mus musculus
1287	129.5	7.2	415	2	060977	060977	mus musculus	1360	125.5	6.9	342	2	P97635	P97635	rattus norv
1288	129.5	7.2	436	2	06VAN8	06VAN8	bos taurus	1361	125.5	6.9	524	2	0810V7	0810v7	bugesia jap
1289	129.5	7.2	582	2	080WM2	080WM2	mus musculus	1362	125.5	6.9	525	2	09W0L9	09w0l9	drosoophila
1290	129.5	7.2	595	2	068SN8	068SN8	mus musculus	1363	125.5	6.9	526	1	BUTRY_HUMAN	013410	homo sapien
1291	129.5	7.2	771	2	08N116	08N116	homo sapien	1364	125.5	6.9	787	2	08K061	08k061	mus musculus
1292	129.5	7.2	967	2	076KE8	076KE8	oncorhynch	1365	125.5	6.9	829	2	09PSV8	09psv8	xenopus lae
1293	129.5	7.2	975	1	KIT_CANPA	07YR7	canis famli	1366	125.5	6.9	975	1	KIT_MOUSE	P05532	mus musculus
1294	129.5	7.2	975	2	08WMN3	08WMN3	canis famli	1367	125.5	6.9	975	2	06QJ87	06qj87	mus musculus
1295	129.5	7.2	979	2	08WMN3	08WMN3	canis famli	1368	125.5	6.9	975	2	07TS86	07ts86	mus musculus
1296	129.5	7.2	987	2	07YZM8	07YZM8	caenorhabdi	1369	125.5	6.9	975	2	08C8K9	08c8k9	mus musculus
1297	129.5	7.2	1040	1	EG15_CABEL	07YR8	caenorhabdi	1370	125.5	6.9	979	2	08C8K9	080Y17	mus musculus
1298	129.5	7.2	1051	2	07JL68	07JL68	caenorhabdi	1371	125.5	6.9	1031	2	080YN7	080yn7	mus musculus
1299	129.5	7.2	1096	2	08MQ14	08MQ14	caenorhabdi	1372	125.5	6.9	10578	2	081SP5	081sf5	caenorhabdi
1300	129	7.1	306	2	09QYL4	09QYL4	mus musculus	1373	125	6.9	370	2	07TSN7	07tsn7	mus musculus
1301	129	7.1	321	2	09DER3	09DER3	gallus gall	1374	125	6.9	398	2	09Y640	09y640	homo sapien
1302	129	7.1	328	2	06ZMC9	06ZMC9	homo sapien	1375	125	6.9	707	2	08CBC6	08cbc6	mus musculus
1303	129	7.1	417	1	PVR_HUMAN	P15151	homo sapien	1376	125	6.9	876	2	07PW78	07pw78	anopheles g
1304	129	7.1	486	2	09DER2	09DER2	gallus gall	1377	125	6.9	964	2	09TQ00	9tq00	sus scrofa
1305	129	7.1	533	2	09DER1	09DER1	gallus gall	1378	125	6.9	977	1	KIT_BOVIN	P43461	bos taurus
1306	129	7.1	1098	1	FGDR_MOUSE	P05622	mus musculus	1379	125	6.9	977	1	KIT_CAPHI	028317	capra hircu
1307	128.5	7.1	213	2	09N167	09N167	papio hamad	1380	125	6.9	1062	2	08AXC7	08axc7	fugu rubrip
1308	128.5	7.1	226	2	07PYC1	07PYC1	anopheles g	1381	125	6.9	1078	2	08AXC8	08axc8	fugu rubrip
1309	128.5	7.1	268	2	046603	046603	sus scrofa	1382	124.5	6.9	145	2	09MZB4	09mzb4	macaca mula
1310	128.5	7.1	477	2	06UXJ4	06UXJ4	homo sapien	1383	124.5	6.9	192	2	09ERP7	09erp7	rattus norv
1311	128.5	7.1	515	2	PVR1_MOUSE	09JKE6	mus musculus	1384	124.5	6.9	244	2	095T89	095t89	drosoophila
1312	128.5	7.1	515	2	06P9M9	06P9M9	mus musculus	1385	124.5	6.9	311	2	06DN73	06dn73	homo sapien
1313	128.5	7.1	595	1	SILL_HUMAN	096P61	homo sapien	1386	124.5	6.9	496	2	06ZT61	06zt61	homo sapien
1314	128.5	7.1	733	2	09QZM7	09QZM7	mus musculus	1387	124.5	6.9	499	2	07Z728	07z728	homo sapien
1315	128	7.1	240	2	06TYZ5	06TYZ5	canis famli	1388	124.5	6.9	504	2	098923	098923	gallus gall
1316	128	7.1	319	2	09TUB0	09TUB0	canis famli	1389	124.5	6.9	731	2	091150	091150	notophthalm
1317	128	7.1	769	2	08N115	08N115	homo sapien	1390	124.5	6.9	828	2	091743	091743	xenopus lae
1318	128	7.1	806	1	FGR3_HUMAN	P22607	homo sapien	1391	124.5	6.9	960	1	KIT_CHICK	008156	gallus gall
1319	128	7.1	1129	2	080UX0	080UX0	mus musculus	1392	124	6.9	259	2	07Z2G1	07z2g1	homo sapien
1320	128	7.1	1214	2	075054	075054	homo sapien	1393	124	6.9	278	2	099232	099232	mus musculus
1321	128	7.1	1427	2	09VZT8	09VZT8	drosoophila	1394	124	6.9	341	2	061354	061354	mus musculus
1322	127.5	7.1	94	2	09VR14	09VR14	bos taurus	1395	124	6.9	426	1	PSG9_HUMAN	000867	homo sapien
1323	127.5	7.1	241	2	007112	007112	bos taurus	1396	124	6.9	650	2	063709	063709	rattus sp.
1324	127.5	7.1	271	1	OX2V_HHV8	P88963	human herpe	1397	124	6.9	812	2	069ZJ6	069zj6	mus musculus
1325	127.5	7.1	271	2	040948	040948	human herpe	1398	124	6.9	972	2	026614	026614	strongyloce
1326	127.5	7.1	339	2	09Z178	09Z178	mus musculus	1399	124	6.9	993	1	FLT3_HUMAN	P16888	homo sapien
1327	127.5	7.1	388	1	BASI_RAT	P26453	rattus norv	1400	124	6.9	999	1	MERK_HUMAN	012865	homo sapien
1328	127.5	7.1	350	2	095KT3	095KT3	macaca fasc	1401	124	6.9	1124	2	06PEL5	06pel5	mus musculus
1329	127.5	7.1	499	1	SIL8_HUMAN	09NY24	homo sapien	1402	124	6.9	1294	2	080T80	080t80	mus musculus
1330	127.5	7.1	926	2	07LDM3	07LDM3	homo sapien	1403	124	6.9	1569	2	06PAC0	06pac0	mus musculus
1331	127	7.0	330	1	CD22_PONPY	09n13	pongo pygma	1404	123.5	6.9	1666	1	MYM1_MOUSE	062234	mus musculus
1332	127	7.0	406	2	08BR70	08BR70	mus musculus	1405	123.5	6.9	181	2	091665	091665	xenopus lae
1333	127	7.0	452	2	070355	070355	mus musculus	1406	123.5	6.8	211	2	08BK18	08bk18	mus musculus
1334	127	7.0	595	2	090720	090720	gallus gall	1407	123.5	6.8	231	2	08WYI6	08wyi6	homo sapien
1335	127	7.0	658	2	08NHN4	08nhn4	homo sapien	1408	123.5	6.8	241	2	06PK61	06pk61	homo sapien
1336	127	7.0	879	1	FLP3_MOUSE	09WV91	mus musculus	1409	123.5	6.8	253	2	09D8H2	09d8h2	mus musculus
1337	127	7.0	992	1	PLT3_MOUSE	000342	mus musculus	1410	123.5	6.8	257	2	08R202	08r202	mus musculus
1338	126.5	7.0	295	2	09ERF5	09erf5	mesocricetu	1411	123.5	6.8	261	2	09D7L8	09d7l8	m. mus muscu
1339	126.5	7.0	305	2	06ZS95	06zS95	homo sapien	1412	123.5	6.8	285	2	09D780	09d780	mus musculus
1340	126.5	7.0	340	2	061349	061349	mus musculus	1413	123.5	6.8	285	2	08V893	08ve93	mus musculus
1341	126.5	7.0	344	2	09UKV4	09ukv4	homo sapien	1414	123.5	6.8	357	2	08SPW5	08spw5	macaca fasc
1342	126.5	7.0	365	1	CXAR_HUMAN	P78310	homo sapien	1415	123.5	6.8	402	2	015227	015227	homo sapien
1343	126.5	7.0	466	2	0956T0	0956T0	drosoophila	1416	123.5	6.8	403	2	08HY15	08hy15	lemur catta
1344	126.5	7.0	516	2	06PHF8	06phf8	brachydanio	1417	123.5	6.8	501	2	06GMJ2	06gmj2	brachydanio
1345	126.5	7.0	677	1	NRG1_XENLA	093383	xenopus lae	1418	123.5	6.8	516	2	06NM94	06nm94	brachydanio

1419	123.5	6.8	574	1	IRL2_MOUSE	Q9e8t7	mus	musculu
1420	123.5	6.8	640	1	DIM1_CAEEL	Q18066	caenorhabdi	
1421	123.5	6.8	645	2	Q6DR98	Q6DR98	mus	musculu
1422	123.5	6.8	978	1	KIT_PELCA	Q28889	felis	salive
1423	123.5	6.8	1349	1	G116_RAT	Q9wvt0	rattus	nory
1424	123	6.8	168	2	Q7Q6K5	Q7Q6K5	anopheles	g
1425	123	6.8	287	2	Q9QW80	Q9QW80	mus	sp. . f
1426	123	6.8	321	2	Q6UX14	Q6ux14	homo	saplen
1427	123	6.8	351	2	Q15225	Q15225	homo	saplen
1428	123	6.8	367	2	Q8T603	Q8T603	drosophi	
1429	123	6.8	399	2	Q9Y279	Q9Y279	homo	saplen
1430	123	6.8	476	2	Q80WU0	Q80WU0	mus	musculu
1431	123	6.8	696	1	IP1L1_HUMAN	Q9anz1	homo	saplen
1432	123	6.8	696	1	IP1L1_PANTR	P60029	pan	trogiod
1433	123	6.8	707	2	P97860	P97860	mus	musculu
1434	123	6.8	821	1	TRKB_MOUSE	P15209	mus	musculu
1435	123	6.8	1072	2	Q8T104	Q8T104	domdyx	mori
1436	123	6.8	1176	2	KML5_BOVIN	Q28824	bos	taurus
1437	122.5	6.8	167	2	Q8NFN2	Q8nf12	homo	saplen
1438	122.5	6.8	211	2	Q7RTW5	Q7rtw5	homo	saplen
1439	122.5	6.8	241	2	Q7RTW0	Q7rtw0	homo	saplen
1440	122.5	6.8	316	1	PCGA_PANTR	Q8epv8	pan	trogiod
1441	122.5	6.8	326	1	VB16_CWXPB	Q04523	compox	viru
1442	122.5	6.8	326	2	Q77DR6	Q77dr6	compox	viru
1443	122.5	6.8	394	2	Q6TGK9	Q6tgk9	oryctolagus	
1444	122.5	6.8	412	2	Q9R1E1	Q9r1e1	rattus	nory
1445	122.5	6.8	462	2	Q7RTW1	Q7rtw1	homo	saplen
1446	122.5	6.8	637	2	Q7RTW3	Q7rtw3	homo	saplen
1447	122.5	6.8	639	2	NRG1_HUMAN	Q02297	h	pro-neure
1448	122.5	6.8	640	2	Q7RTV8	Q7rtv8	homo	saplen
1449	122.5	6.8	645	2	Q7RTW4	Q7rtw4	homo	saplen
1450	122.5	6.8	662	1	NRG1_RAT	P43322	r	pro-neure
1451	122.5	6.8	785	2	Q7TNP4	Q7tnp4	mus	musculu
1452	122.5	6.8	994	1	MERK_RAT	P57097	rattus	nory
1453	122	6.8	272	2	Q8R1N5	Q8r1n5	mus	musculu
1454	122	6.8	390	2	Q7Q6R2	Q7q6r2	anopheles	g
1455	122	6.8	397	2	Q09263	Q09263	cercopithec	
1456	122	6.8	458	1	CD4_MACFA	P79185	macaca	fasc
1457	122	6.8	459	2	Q6ZMD0	Q6zmd0	homo	saplen
1458	122	6.8	606	2	Q9BZ20	Q9bz20	homo	saplen
1459	122	6.8	696	1	IP1L1_FONPY	Q7Yq19	pongo	pygma
1460	122	6.8	696	1	IP1L1_RAT	P59824	rattus	nory
1461	122	6.8	850	1	NRG2_HUMAN	Q14511	homo	saplen
1462	122	6.8	923	2	Q97745	Q97745	mus	scrofa
1463	122	6.8	953	2	Q6P6Y9	Q6p6y9	xenopus	lae
1464	122	6.8	964	2	Q97744	Q97744	mus	scrofa
1465	122	6.8	964	2	Q97Q01	Q97q01	mus	scrofa
1466	122	6.8	1685	2	Q6H969	Q6h969	homo	saplen
1467	122	6.8	1685	2	Q6ZU00	Q6ZU00	homo	saplen
1468	121.5	6.7	155	2	Q9J317	Q9j317	mus	musculu
1469	121.5	6.7	305	2	Q6PJ00	Q6pj00	homo	saplen
1470	121.5	6.7	332	1	PSGB_HUMAN	Q9qj72	homo	saplen
1471	121.5	6.7	365	2	Q8MWV3	Q8mwv3	bos	taurus
1472	121.5	6.7	390	2	Q96AP7	Q96ap7	homo	saplen
1473	121.5	6.7	390	2	Q96T50	Q96t50	homo	saplen
1474	121.5	6.7	412	2	Q63611	Q63611	rattus	nory
1475	121.5	6.7	558	2	Q6PDS1	Q6pds1	homo	saplen
1476	121.5	6.7	637	2	Q6NSG0	Q6nsg0	homo	saplen
1477	121.5	6.7	818	1	TRKB_CHICK	Q91987	gallus	gall
1478	121.5	6.7	821	1	TRKB_RAT	Q66504	rattus	nory
1479	121.5	6.7	1450	1	MESE_CHICK	Q02173	gallus	gall
1480	121	6.7	223	2	Q9NBO0	Q9nbo0	drosophi	
1481	121	6.7	277	2	Q61RE8	Q61re8	rattus	nory
1482	121	6.7	281	2	P97546	P97546	rattus	nory
1483	121	6.7	292	2	Q9N168	Q9n168	papio	hamad
1484	121	6.7	292	2	Q57146	Q57146	human	herpe
1485	121	6.7	292	2	Q785L7	Q785L7	human	herpe
1486	121	6.7	303	2	Q7ZXR4	Q7zxrx	xenopus	lae
1487	121	6.7	305	2	Q6P3A4	Q6p3a4	mus	musculu
1488	121	6.7	532	2	Q95R30	Q95r30	drosophi	
1489	121	6.7	733	2	Q6O830	Q6o830	mus	musculu
1490	121	6.7	733	2	Q80T10	Q80t10	mus	musculu
1491	121	6.7	994	1	MERK_MOUSE	Q60805	mus	musculu

1492	121	6.7	1035	2	Q9NEG1	Q9neg1	drosophi	
1493	121	6.7	1142	1	MYPF_HUMAN	Q14324	homo	saplen
1494	121	6.7	1333	2	Q7P5T7	Q7p5t7	anopheles	g
1495	120.5	6.7	284	2	Q9NX42	Q9nx42	homo	saplen
1496	120.5	6.7	316	2	Q8VE98	Q8ve98	mus	musculu
1497	120.5	6.7	316	2	Q7TPB4	Q7tpb4	rattus	nory
1498	120.5	6.7	353	2	Q63242	Q63242	rattus	nory
1499	120.5	6.7	461	2	Q35947	Q35947	mesocricetu	
1500	120.5	6.7	468	2	Q6PJ50	Q6pj50	mus	musculu

ALIGNMENTS

RESULT 1

Q8BG33	PRELIMINARY;	PRT;	344 AA.
AC	Q8BG33;		
DT	01-MAR-2003 (TREMBLrel. 23, Created)		
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)		
DT	05-JUN-2004 (TREMBLrel. 27, Last annotation update)		
DE	mus musculi adult male corpora quadrigemina cDNA, RIKEN full-length		
DE	enriched library, clone: B230328N06 product: NEURORTRIMIN (GP65) homolog		
DE	(mus musculi adult male corpora quadrigemina cDNA, RIKEN full-length		
DE	enriched library, clone: B230377K17 product: NEURORTRIMIN (GP65)		
DE	homolog).		
GN	Name: Hnt;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;		
RX	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;		
RA	Carninci P., Hayashizaki Y.;		
RT	"High-efficiency full-length cDNA cloning.";		
RL	Mech. Enzymol. 303:19-44(1999).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;		
RX	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;		
RA	RIKEN FANTOM Consortium;		
RT	"Functional annotation of a full-length mouse cDNA collection.";		
RL	Nature 409:685-690(2001).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;		
RA	The FANTOM Consortium,		
RT	the RIKEN Genome Exploration Research Group Phase I & II Team;		
RL	"Analysis of the mouse transcriptome based on functional annotation of		
RT	60,770 full-length cDNAs.";		
RL	Nature 420:563-573(2002).		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;		
RX	MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.154100;		
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,		
RT	Komoto H., Okazaki Y., Muramatsu M., Hayashizaki Y.;		
RL	"Normalization and subtraction of cap-trapper-selected cDNAs to		
RT	prepare full-length cDNA libraries for rapid discovery of new genes.";		
RL	Genome Res. 10:1617-1630(2000).		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;		
RX	MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;		
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,		
RT	Komoto H., Akiyama J., Nishi K., Kitanai T., Tashiro H., Itoh M.,		
RL	Sunmi N., Ishii Y., Nakamura S., Hazama M., Mashino T., Harada A.,		
RT	Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,		
RL	Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,		
RA	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,		
RA	Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;		

RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).
 RN [6]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RA Aachai J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Horii P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohnato N., Okazaki Y.,
 RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK045973; BAC32555.1; -
 DR EMBL; AK046377; BAC32695.1; -
 DR HSSP; P13596; I021.
 DR MGD; MGI:2446259; Hnt.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; Ig_c2.
 DR Pfam; PF00047; Ig_2.
 DR SMART; SM00408; Igc2_2.
 DR PROSITE; PSS00835; IG_LIKE; 3.
 SQ SEQUENCE 344 AA; 37941 MW; CDA5299D4CD86065 CRC64;

Query Match 98.6%; Score 1780; DB 2; Length 344;
 Best Local Similarly 98.0%; Pred. No. 1.5e-13;
 Matches 337; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKTIQPMHNSISAIPTGLALCLFGVPRSGDAPPRAMDVTVRQGESATLRCTID 60
 DB 1 MKTIQPMHNSISAIPTGLALCLFGVPRSGDAPPRAMDVTVRQGESATLRCTID 60

QY 61 NRTYVAMLRSTLYVANDKMCIDPRVLLSNTQYYSIEIQVNDVYDGGPYTCVQTD 120
 DB 61 NRTYVAMLRSTLYVANDKMCIDPRVLLSNTQYYSIEIQVNDVYDGGPYTCVQTD 120

QY 121 NHRKTSVHLIVQVSPKIVISSDISINEGNISLCTIAGRPPTTMRHSKANGFV 180
 DB 121 NHRKTSVHLIVQVSPKIVISSDISINEGNISLCTIAGRPPTTMRHSKANGFV 180

QY 181 SEDEYLEIGITRQSGDYECASANDVAAPVVRKVTVMVPPYISRAKGTGVGQGT 240
 DB 181 SEDEYLEIGITRQSGDYECASANDVAAPVVRKVTVMVPPYISRAKGTGVGQGT 240

QY 241 LQCEASAVPSAEFQWYDKRLIEGKKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300
 DB 241 LQCEASAVPSAEFQWYDKRLIEGKKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNK 300

QY 301 LGHTNASIMLPGPQAVSEVSNSTRRAGCWLPLVLHLILKF 344
 DB 301 LGHTNASIMLPGPQAVSEVSNSTRRAGCWLPLVLHLILKF 344

RESULT 2
 NTRI_HUMAN STANDARD; PRT; 344 AA.
 AC Q9P121; Q6UXJ3; Q86VJ9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Neurotrophin precursor (hnt) (UNQ297/PRO337).
 GN Name=NT;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).

RA Li G., Jin J., Tan X., Hu S., Yuan J., Qiang B.;
 RT "Cloning and identification of human neurotrophin full length cDNA."
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC MEDLINE=22867236; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S.,
 RA Hang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis I., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J.,
 RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vages A.,
 RA Vanden R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P., Gray A.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment."
 RL Genome Res. 13:2265-2270(2003).
 RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Krausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow R.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulian S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fehey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalak U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]

RP SEQUENCE OF 34-48.
 RX PubMed=15340161; DOI=10.1101/ps.04682504;
 RA Zhang Z., Henzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites."
 RL Protein Sci. 13:2819-2824(2004).
 CC -1- FUNCTION: Neural cell adhesion molecule.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q9P121-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9P121-2; Sequence=VSP_010939;
 CC Note=No experimental confirmation available;
 CC Name=3;
 CC IsoId=Q9P121-3; Sequence=VSP_010940, VSP_010941;
 CC Note=No experimental confirmation available;
 CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. IGLON
 CC family.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -----
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CC -----
DR EMBL; AF126426; AAF37591.1; -
DR EMBL; AY358331; AAO8697.1; -
DR EMBL; BC050716; AAH50716.1; -
DR HSBP; F13590; I1E5.
DR MIM; 607938; -
DR GO; GO:0008038; P:neuronal cell recognition; TAS.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00408; IgC2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Alternative splicing; Cell adhesion; Direct protein sequencing;
KW Glycoprotein; GPI-anchor; Immunoglobulin domain; Lipoprotein; Repeat;
KW Signal.
FT SIGNAL 1 33
FT CHAIN 34 321
FT PROPEP 322 344
FT DOMAIN 39 126
FT DOMAIN 136 218
FT DOMAIN 222 309
FT DISULFID 57 115
FT DISULFID 157 201
FT CARBOHYD 243 295
FT CARBOHYD 44 44
FT CARBOHYD 70 70
FT CARBOHYD 152 152
FT CARBOHYD 284 284
FT CARBOHYD 292 292
FT CARBOHYD 305 305
FT CARBOHYD 321 321
FT LIPID 321 321
FT VAAPSLIC 1 27
FT VAAPSLIC 313 316
FT VAAPSLIC 317 344
FT VAAPSLIC 344 AA; 37971 MW; DAAD12C295ABBE3A CRC64;
SQ SEQUENCE 344 AA; 37971 MW; DAAD12C295ABBE3A CRC64;
Query Match 92.2%; Score 1665.5; DB 1; Length 344;
Best Local Similarity 95.2%; Pred. No. 1,9e-124;
Matches 320; Conservative 3; Mismatches 10; Indels 3; Gaps 1;
QY 12 ISMAIFGTGLALCLF--QGVVPSGDTFPKAMDNVTVRQGESATLCTIDNRVTRVAM 68
DB 9 LPMKCLVVVSLRLFLVPTGVPSGDTFPKAMDNVTVRQGESATLCTIDNRVTRVAM 68
QY 69 LNRSTILVAGNDKCLDPRVVLSTQVYSIEIONDVYDEGPTGCVQTDNHPKTSRV 128
DB 69 LNRSTILVAGNDKCLDPRVVLSTQVYSIEIONDVYDEGPTGCVQTDNHPKTSRV 128
QY 129 HLIYQVSPKIYVIESDISINEGNNISLCTIATGPREPTVTRHISPKAVGVSEDEYLEI 188
DB 129 HLIYQVSPKIYVIESDISINEGNNISLCTIATGPREPTVTRHISPKAVGVSEDEYLEI 188
QY 189 QGITREGSGDYECASNDVAAPVVRVRYVYVPPYISSEAKGTGVPQKGTLOCEASAV 248
DB 189 QGITREGSGDYECASNDVAAPVVRVRYVYVPPYISSEAKGTGVPQKGTLOCEASAV 248
QY 249 PSARFQWKDKRLIEGKGVKVENRPLSLIPNVSEHYGNTCVASKLGHNTASI 308
DB 249 PSARFQWKDKRLIEGKGVKVENRPLSLIPNVSEHYGNTCVASKLGHNTASI 308
QY 309 MLFGGAVSEVNGTSRRAGCWMLLPLVLHLHLKF 344
DB 309 MLFGGAVSEVNGTSRRAGCWMLLPLVLHLHLKF 344
RESULT 3
NTRI_MOUSE

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ID NTRI_MOUSE STANDARD; PRT; 344 AA.
AC Q99P70;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Neurotictin precursor.
GN Name=Nt; Synonyms=Hnt;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Brain;
RA Kim T.H., Choi S.C., Kim J., Jeon J.W., Kim K.D., Lee S.H.;
RT "Cloning and expression of mouse neurotictin gene in the developing
RL nervous system."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
[2]
RC SEQUENCE FROM N.A.
RA STRAIN=C57BL/6; TISSUE=B-eye;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Mansueti K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshimiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loguailano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heaton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.M., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhe U.A.;
RA Scherch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Neural cell adhesion molecule.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON
CC family.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -----
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CC or send an email to license@1db-61b.ch).
CC -----
DR EMBL; AF282980; AAK00276.1; -
DR EMBL; BC023307; AAH23307.1; -
DR MGD; MGI:2446259; Hnt.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00408; IgC2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Cell adhesion; Glycoprotein; GPI-anchor; Immunoglobulin domain;
KW Lipoprotein; Repeat; Signal.
FT SIGNAL 1 33
FT CHAIN 34 321
FT PROPEP 322 344
FT DOMAIN 39 126
FT DOMAIN 136 218
FT DOMAIN 222 309
FT DISULFID 57 115

```

FT DISULFID 157 201 Potential.
 FT DISULFID 243 295 Potential.
 FT CARBOHYD 44 44 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 70 70 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 152 152 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 284 284 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 292 292 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 305 305 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 321 321 N-linked (GlcNAc. . .) (Potential).
 FT LIPID 321 321 GPI-anchor amidated asparagine (Potential).
 FT CONFLICT 75 75 I -> P (in Ref. 1).
 FT CONFLICT 92 92 S -> G (in Ref. 1).
 FT CONFLICT 119 119 T -> I (in Ref. 1).
 FT CONFLICT 187 187 E -> Q (in Ref. 1).
 FT CONFLICT 213 213 R -> P (in Ref. 1).
 FT CONFLICT 225 225 I -> F (in Ref. 1).
 SQ SEQUENCE 344 AA; 37984 MW; C985BBA52C146554 CRC64;

Query Match 91.2%; Score 1647.5; DB 1; Length 344;
 Best Local Similarity 93.5%; Pred. No. 5.3e-123;
 Matches 314; Conservative 8; Mismatches 11; Indels 3; Gaps 1;

QY 12 ISWALFTGLALCLF---QGVPRSGDAPPKAMDNTVVGSGSATLRCTIDNRVTVAV 68
 DB 9 LPMKCLVVSRLRLFLVPTGVPVSSGDATPPKAMDNTVVGSGSATLRCTIDNRVTVAV 68
 QY 69 LNSTSTLYAGNDKWCCLDPVRVLLSNTQYSEIQNVVDYDEGPTCSVQTDNHPKTSRV 128
 DB 69 LNSTSTLYAGNDKWCCLDPVRVLLSNTQYSEIQNVVDYDEGPTCSVQTDNHPKTSRV 128
 QY 129 HLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVWRHISPAVGFVSEDEYLEI 188
 DB 129 HLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVWRHISPAVGFVSEDEYLEI 188
 QY 189 OGITREOSGDYECASANDVAAPVRRKVTVPYPISEAKGTGVPVGQGTIQCEASAV 248
 DB 189 OGITREOSGDYECASANDVAAPVRRKVTVPYPISEAKGTGVPVGQGTIQCEASAV 248
 QY 249 PSAEFQWYKDDKRLIEGKGVKVENRPPSLKLIFFNVSEHDYNYTCVANSKLGHTNASI 308
 DB 249 PSAEFQWYKDDKRLIEGKGVKVENRPPSLKLIFFNVSEHDYNYTCVANSKLGHTNASI 308
 QY 309 MLFGPGAVSEVSNCTSRACGCVLLPLVYLHLILKF 344
 DB 309 MLFGPGAVSEVSNCTSRACGCVLLPLVYLHLILKF 344

RESULT 4
 NTRI_RAT STANDARD; PRT; 344 AA.
 ID NTRI_RAT
 AC Q62718;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Neurotrophin precursor (Gp65).
 GN Name=Nt;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 217-229.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=95198094; PubMed=7891157;
 RA Stryck A.F., Canoll P.D., Wolfgang M.J., Rosen C.L., D'Buschachio P.,
 RA Salzer J.L.;
 RT "Cloning of neurotrophin defines a new subfamily of differentially
 RT expressed neural cell adhesion molecules.";
 RL J. Neurosci. 15:2141-2156(1995).
 CC -1- FUNCTION: Neural cell adhesion molecule.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- TISSUE SPECIFICITY: Central nervous system.

CC -1- DEVELOPMENTAL STAGE: Expressed at high levels in several
 CC developing projection systems: in neurons of the thalamus,
 CC subplate, and lower cortical laminae in the forebrain and in the
 CC pontine nucleus, cerebellar granule cells, and Purkinje cells in
 CC the hindbrain.
 CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON
 CC family.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
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 CC -----

DR EMBL, U16845; AAA67445.1; -.
 DR PIR, I56551; I56551.
 DR InterPro, IPR007110; Ig-like.
 DR InterPro, IPR003598; Ig_c2.
 DR Pfam, PF00047; Ig_3.
 DR SMART, SM00408; IGC2; 2.
 DR PROSITE, PSS0835; IG_LIKE; 3.
 KW Cell adhesion; Direct protein sequencing; Glycoprotein; GPI-anchor;
 KW Immunoglobulin domain; Lipoprotein; Repeat; Signal.
 FT SIGNAL 1 33 Potential.
 FT CHAIN 34 321 Neurotrophin.
 FT PROPEP 322 344 Removed in mature form (Potential).
 FT DOMAIN 39 126 Ig-like C2-type 1.
 FT DOMAIN 136 218 Ig-like C2-type 2.
 FT DOMAIN 222 309 Ig-like C2-type 3.
 FT DISULFID 57 115 Potential.
 FT DISULFID 157 201 Potential.
 FT DISULFID 243 295 Potential.
 FT CARBOHYD 44 44 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 70 70 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 152 152 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 216 216 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 284 284 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 292 292 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 305 305 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 321 321 N-linked (GlcNAc. . .) (Potential).
 FT LIPID 321 321 GPI-anchor amidated asparagine (Potential).
 SQ SEQUENCE 344 AA; 37998 MW; CB839B853B33224 CRC64;

Query Match 90.8%; Score 1639.5; DB 1; Length 344;
 Best Local Similarity 92.9%; Pred. No. 2.3e-122;
 Matches 312; Conservative 9; Mismatches 12; Indels 3; Gaps 1;

QY 12 ISWALFTGLALCLF---QGVPRSGDAPPKAMDNTVVGSGSATLRCTIDNRVTVAV 68
 DB 9 LPMKCLVVSRLRLFLVPTGVPVSSGDATPPKAMDNTVVGSGSATLRCTIDNRVTVAV 68
 QY 69 LNSTSTLYAGNDKWCCLDPVRVLLSNTQYSEIQNVVDYDEGPTCSVQTDNHPKTSRV 128
 DB 69 LNSTSTLYAGNDKWCCLDPVRVLLSNTQYSEIQNVVDYDEGPTCSVQTDNHPKTSRV 128
 QY 129 HLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVWRHISPAVGFVSEDEYLEI 188
 DB 129 HLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVWRHISPAVGFVSEDEYLEI 188
 QY 189 OGITREOSGDYECASANDVAAPVRRKVTVPYPISEAKGTGVPVGQGTIQCEASAV 248
 DB 189 OGITREOSGDYECASANDVAAPVRRKVTVPYPISEAKGTGVPVGQGTIQCEASAV 248
 QY 249 PSAEFQWYKDDKRLIEGKGVKVENRPPSLKLIFFNVSEHDYNYTCVANSKLGHTNASI 308
 DB 249 PSAEFQWYKDDKRLIEGKGVKVENRPPSLKLIFFNVSEHDYNYTCVANSKLGHTNASI 308
 QY 309 MLFGPGAVSEVSNCTSRACGCVLLPLVYLHLILKF 344
 DB 309 MLFGPGAVSEVSNCTSRACGCVLLPLVYLHLILKF 344

Db 309 MLFGAVSEVNGSTRRAGCIWLLPLVLHLKLF 344

RESULT 5

CEPU-CHICK STANDARD; PRT; 353 AA.

AC Q90773; (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE CEPU-1 protein precursor.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

NCBI_TaxID=9031;

OX NCBI

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC TISSUE=Brain;

RX MEDLINE=96370549; PubMed=8774445;

RA Spaltemann F.; Brummendorf T.;

RT "CEPU-1, a novel immunoglobulin superfamily molecule, is expressed by developing cerebellar Purkinje cells.";

RL J. Neurosci. 16:1170-1179 (1996).

CC -1- FUNCTION: It may be a cellular address molecule specific to Purkinje cells. It may represent a receptor or a subunit of a receptor complex.

CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named Isoforms=2;

CC Name=1; Synonyms=Minor;

CC IsoId=Q90773-1; Sequence=Displayed;

CC Name=2; Synonyms=Major;

CC IsoId=Q90773-2; Sequence=VSP_002607;

CC -1- TISSUE SPECIFICITY: Found on the dendrites, somata and axons of developing Purkinje cells. Undetectable on other neurons like Golgi or granule cells.

CC -1- DEVELOPMENTAL STAGE: Expressed by developing cerebellar Purkinje cells. Expression coincides with the growth of the dendritic tree, after Purkinje cells have finished their migration from the ventricular zone (from E15 until E21). Expressed in the adult.

CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLOn family.

CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

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CC -----

DR EMBL; 272497; CAA96578.1; -

DR InterPro; IPR007110; Ig-1like.

DR InterPro; IPR003598; Ig_c2.

DR Pfam; PR00047; Ig_3; 2.

DR SMART; SM00408; IGC2; 2.

DR PROSITE; PS50835; IG_LIKE; 3.

DR Alternative splicing; Cell adhesion; Glycoprotein; GPI-anchor; Immunoglobulin domain; Lipoprotein; Repeat; Signal.

KM Immunoglobulin domain; Lipoprotein; Repeat; Signal.

FT SIGNAL 1 28

FT CHAIN 29 330

FT PROPEP 331 353

FT DOMAIN 337 124

FT DOMAIN 337 124

FT DOMAIN 337 124

FT DOMAIN 337 124

FT DISULFID 55 113

FT DISULFID 155 199

FT DISULFID 241 293

FT CARBOHYD 42 42

FT CARBOHYD 68 68

FT CARBOHYD 150 150

FT CARBOHYD 282 282 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 290 290 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 303 303 N-linked (GlcNAc...) (Potential).

FT LIPID 330 330 GPI-anchor amidated serine (Potential).

FT VARSPLIC 310 320 Missing (in isoform 2).

FT FT

FT SQ SEQUENCE 353 AA; 38736 MW; 2550C48591EBBBA6 CRC64;

Query Match 81.8%; Score 1477.5; DB 1; Length 353;

Best Local Similarity 78.6%; Pred. No. 2e-109;

Matches 276; Conservative 32; Mismatches 32; Indels 11; Gaps 1;

Qy 5 QPKHNSISWAFITGLAALCLFGVPPVRSQDAPPKAMNDVTVQGSASATRCITDNT 64

Db 3 QAKQHPPSWITFAGMALLLFGVPPVRSQDAPPKAMNDVTVQGSASATRCITDNT 62

Qy 65 RVAMLNSTIIYAGNDKCLDPVYVLSNTOTQYISLQNDVYDDEGYTSCVTDNHPK 124

Db 63 RVAMLNSSIIYAGNDKCLDPVYVLSNTOTQYISLQNDVYDDEGYTSCVTDNHPK 122

Qy 125 TSVVHLIVQVSPKIVISDISISIEGNNISLTCTATGPRPPTVTRHISPAVGSBDE 184

Db 123 TSVVHLIVQVSPKIVISDISISIEGNNISLTCTATGPRPPTVTRHISPAVGSBDE 182

Qy 185 YLEITQITREGSGDYECSSANDVAAPVVRKVTVNTPPYISBAKGTGVPVGOKTQCE 244

Db 183 YLEITQITREGSGDYECSSANDVAAPVVRKVTVNTPPYISBAKGTGVPVGOKTQCE 242

Qy 245 ASAVPSAEFQWYKODKRLISGKGVKVENRPFSLKLIFFNVSEHDYGYTVAANKLGH 304

Db 243 ASAVPSAEFQWYKODKRLISGKGVKVENRPFSLKLIFFNVSEHDYGYTVAANKLGH 302

Qy 305 NASIMLF-----GPGAVSEVNGSTRRAGCIWLLPLVLHLKLF 344

Db 303 NASIMLYEITTTALTTPMKFGAVHDGNSGAMRRKSCAWLLPLVLHLKLF 353

RESULT 6

ID 057596 PRELIMINARY; PRT; 313 AA.

AC 057596;

DT 01-JUN-1998 (TREMBLrel. 06, Created)

DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)

DT 05-JUN-2004 (TREMBLrel. 27, Last annotation update)

DE Neural secreted glycoprotein (CEPU-Se alpha 2 isoform).

GN Name=CEPU; Synonyms=CEPU-Se;

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

NCBI_TaxID=9031;

OX NCBI

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96347334; PubMed=10420985;

RA Kim D.S.; Rhew T.H.; Moss D.J.; Kim J.Y.;

RT "cDNA cloning of the CEPU5, a secreted type of neural glycoprotein belonging to the immunoglobulin-like oploid binding cell adhesion molecule (OB CAM) subfamily.";

RL Mol. Cells 9:270-276 (1999).

RN [2]

RP SEQUENCE FROM N.A.

RA Kim D.;

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Lodge A.P.; McNamee C.J.; Howard M.R.; Reed J.B.; Moss D.J.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ225897; CAA12649.1; -

DR EMBL; AF292935; AAC01878.1; -

DR HSSP; Q9U0H9; IDUS.

DR InterPro; IPR007110; Ig-1like.

DR InterPro; IPR003598; Ig_c2.

DR Pfam: PF00047; Ig 2.
DR SMART: SM00408; IGG2, 2.
DR PROSITE: PS50835; IG LIKE, 3.
SQ SEQUENCE 313 AA; 34482 MW; 99ADB25CAE4A5347 CRC64

Query Match	79.1%	Score 1438	DB 2	Length 313
Best local Similarity	85.4%	Pred. No. 1.5e-105		
Matches 263	Conservative 27	Mismatches 18	Indels 0	Gaps 0

[illegible]

RESULT 7	
093242	
ID 093242	PRELIMINARY; PRT; 344 AA.

DT DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE CESPu-1.
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neoognathae; Galliformes; Psittacidae; Psittacinae;
OC Gallus.
OX NCBI_TaxId=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura Y., Shirabe K., Fukushima M., Takeshita M., Tanaka H.,
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB01810; BAA1514.1; -.
DR HSPB; Q90QH9; IDJ5.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR03598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PSS0835; IG_LIKE; 3.
SQ SEQUENCE 344 AA; 37613 MW; 22CAAF526A6B57E CRC64;

Query Match	79.0%	Score 1427.5	DB 2	Length 344
Best Local Similarity	79.2%	Pred. No. 1.8e-105		
Matches 267	Conservative 31	Mismatches 36	Indels 3	Gaps 1

OY 11 S I M A F T G L A A C E --- Q G V P S G D A T F P K A N D N T Y R Q S S A T R C I D I N D R Y R V A 67
:
:
:
D b 8 A L P M R C L V L C I R L F L Y P A G V P V R S G D A T F P K A N D N T Y R Q S S A T R C I S V D N R Y T R V A 67
:
:
:
OY 68 W I N R S I L L A G N D K W C L D P R V Y L L S N T O Q V S I E I Q N D V Y D E B P T Y C S V O T D N H P T S R 127
:
:
:
D b 68 W I N R S I L L A G N D K C L D P R V Y L L S N T O Q V S I Q I H D V D V D E G Y T C S V O T D N H P T S R 127
:
:
:
OY 128 V H L I V O S P K I E I S S D I S I N E G N N I S L T C I A T G R P E F T V W R H I S P R A G V S E D E Y L E 187
:

Db 128 VHLIYGVSKRIEISDSDISINEGGVSLTCLATRPDPTITMNRHSKAVGFISEBYLE 187
 QY 188 IOGITREDSGDYECASANDVAAPVVRKRVKTVNYPYIISBAKGTGVGVQKGLTCEASA 247
 Db 188 ITGITREBSGEYECASNDVAAPVVGKRVKTVNYPYISDAKSTGVGVQKGLTCEASA 247
 QY 248 VPSAEFQWYKDDKRLLEGGKGVYENRPLSKLIFPNVSEHDYGNITCVASNTLGHNTAS 307
 Db 248 VPSADPQWYKDDKRLAEGGKGLKYNKAFPSRLIFPNVSEBDYGNITCVASNTLGHNTAS 307
 QY 308 IMLFGAVSEVSNGTSPRAGCWLILPLLVLHLLIKP 344
 Db 308 MLTYGVAHNDGNSGAMWRGSCAMLLALPLAQLARQF 344

RESULT 8	
09DGI5	
ID 09DGI5	PRELIMINARY;
DATE	PRT; 315 AA

DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE CEFU-se alpha 1 isoform.
 GN Name=CEFU-Se;
 OS Gallus gallus (chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae
 OC Gallus.
 OX NCBI_TaxId=9031,
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Lodge A.P., McNamee C.J., Howard M.R., Reed J.E., Moss D.J.;
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF292936; AAC01879.1; -.
 DR HSSP; Q9UQH9; IDSJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_cd.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00408; IGC2; 2.
 DR PROSITE; PSS0835; IG_LIKE; 3.
 QO SEQUENCE 315 AA; 34606 MW; 68CSD27F0DDC6FB2 CRC64;

Query Match	75.2%	Score 1357.5	DB 2	Length 315
Best Local Similarity	83.0%	Pred. No. 6	2e-100	
Matches 253, Conservative	26	Mismatches	23	Indels 3
				Gaps 1

Qy	12	SISMAFTGLALCF---	OGPVASGATPEPKAMDNVYVROGSATLPTCINRVTYVA	67
		:::		
Db	8	ALPMRCVLVLCRIILFLYV	PVAVASGATPEPKAMDNVYVROGSATLPTCINRVTYVA	67
Qy	68	MLNRSTIILVAGNDKMC	DPVVLVLSNTOTQYSIEIQNDVYDEBPYTCSVOTDNHPETSR	127
Db	68	MLNRSTIILVAGNDKMC	DPVVLVLSNTOTQYSIEIQNDVYDEBPYTCSVOTDNHPETSR	127
Qy	128	VHLIVQSPKIVEISSDIS	INEGNNISLTCTATGRPEPTVWRHISPKAVGVSEDEYLE	187
Db	128	VHLIVQSPKIVEISSDIS	INEGNNISLTCTATGRPEPTVWRHISPKAVGVSEDEYLE	187
Qy	188	IOGITREOSGDYECAS	NDVAAPVVRVRYKVTVNTPTPIYISAKGTGVPVGOGKITLQCEASA	247
Db	188	ITGITREOSGEYECAS	NDVAAPVVRVRYKVTVNTPTPIYISAKGTGVPVGOGKITLQCEASA	247
Qy	248	VPSAEQWTKDKNKL	IEKKGVKYVENRPFSLKLLFPVNSEHDYENYTCVASNQLGHNNAS	307
Db	248	VPSAEQWTKDKNKL	IEKKGVKYVENRPFSLKLLFPVNSEHDYENYTCVASNQLGHNNAS	307
Qy	308	IMLFG	312	
		:::		
Db	308	IMLFG	312	


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RESULT 9
ID 06DFY2 PRELIMINARY; PRT; 337 AA.
AC 06DFY2:
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein 3732419F12.
GN Name=3732419F12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosnak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
RA Krzyzanski M.I., Shalaka U., Smallos D.E., Scherch A., Schin J.E.,
RA Jones S.J., Maitra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Director MGC Project;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC076581; AAH76581.1; -
DR InterPro; IPR003599; IG_1.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG_3.
DR SMART; SM00409; IG_3.
DR SMART; SM00408; IGc2; 3.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Hypothetical protein_3732419F12; 24279D982E60F4AB CXC64;
SQ SEQUENCE 337 AA; 37156 MW; 2A279D982E60F4AB CRC64;

Query Match 72.3%; Score 1306; DB 2; Length 337;
Best Local Similarity 72.1%; Pred. No. 8.6e-96;
Matches 243; Conservative 35; Mismatches 59; Indels 0; Gaps 0;

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OY 248 VPSAEFQWYXDDKELLEGKGVKVENRPFSLKLFVNVSEHDYGNVCVANSKLGHTNAS 307
DB 241 VPMAEFQWYXDDKELLEGKGVKVENRPFSLKLFVNVSEHDYGNVCVANSKLGHTNAS 300
OY 308 IMFPGAVSEVNGSTRAGCWLPLVLAHLIKF 344
DB 301 IITLYGPAVIDGVNASRALLCWLSTGFPAHFPIKF 337

RESULT 10
ID 06CM_CHICK STANDARD; PRT; 337 AA.
AC 06CM_CHICK:
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Opioid binding protein/cell adhesion molecule homolog precursor
DE (Neurite inhibitor GP55-A) (OBGM protein gamma isoform).
GN Name=OBGM;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Lodge A.P., Kim D.-S., Howard M.R., McNamee C.J., Smith N., Moss D.J.;
RT "Cloning of CEPU-8, a secreted isoform of CEPU-1, and OBGM cDNAs from
RT chick: structural diversity of IgLON family proteins."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 64-337 FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=97157768; PubMed=904047;
RA Wilson D.J.A., Kim D.-S., Clarke G.A., Marshall-Clarke S., Moss D.J.;
RT "A family of glycoproteins (GP55), which inhibit neurite outgrowth,
RT are members of the Ig superfamily and are related to OBGM,
RT neurotrophin, LAMP and CEPU-1."
RL J. Cell Sci. 109:3129-3138(1996).
CC -1- FUNCTION: Inhibits neurite outgrowth.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- TISSUE SPECIFICITY: Restricted to the nervous system.
CC -1- DEVELOPMENTAL STAGE: Increases during development from very low
CC levels at embryonic day 10 and is most abundant after hatching.
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. IGLON
CC family.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y08170; CAB41420.1; -
DR HSSP; P78310; IFSW.
DR InterPro; IPR007110; IG_1like.
DR Pfam; PF00047; IG_3.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Cell adhesion; Direct protein sequencing; Glycoprotein; GPI-anchor;
KW Immunoglobulin domain; Lipoprotein; Membrane; Repeat; Signal.
FT CHAIN 1 20
FT SIGNAL 21 314
FT PROPEP 315 337
FT DOMAIN 32 119
FT DOMAIN 129 211
FT DOMAIN 215 302
FT DISULFID 50 108
FT DISULFID 150 194
FT POTENTIAL 194

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FT DISULFID 236 288 Potential.
 FT LIPID 314 314 GPI-anchor amidated asparagine
 FT CARBOHYD 133 133 (Potential).
 FT CARBOHYD 277 277 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 285 285 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 298 298 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 337 AA; 36887 MW; BAE71755185651E CRC64;

Query Match 72.3%; Score 1305; DB 1; Length 337;
 Best Local Similarity 73.2%; Pred. No. 1e-95;
 Matches 248; Conservative 34; Mismatches 53; Indels 4; Gaps 2;

QY MHNSISMAIFGTALCLFPGVPRSGDATPPKAMDNVTVRQGESATLRTCTIDRVRVA 67
 DB 1 MYHPACIVFETATALLFIFGVPRSGDATPPKAMDNVTVRQGESATLRTCTIDRVRVA 60
 QY 68 WLRSTLLVAGNDKWCIDPRVLLSNTQYSIEIQNVVDYDEGPYCSVQTDNHPKTSR 127
 DB 61 WLRSTLLVAGNDKWSIDNRVLLSNTKQYSIKIHNVVDYDEGPYCSVQTDNHPKTSR 120
 QY 128 VHLIVQSPKIVEISSDISINEGNNISLTCTIATGRPEPTVTHRISPKAVFVSEDEYLE 187
 DB 121 VHLIVQSPQIVTSSDITVNEGSSVTLMLCLAFGRPEPTVTHRLSGKGFVSEDEYLE 180
 QY 188 IQGITREOSGDYECASNDVAAPVVRKYTVNTPYISAKGTGVPVGOKTLOCEASA 247
 DB 181 ITGITREOSGEYECASNDVAAPVVRKYTVNTPYISAKGTGVPVGOKTLOCEASA 240
 QY 248 VPSAEFQWYKDDRLIEGKKGVKVENRPLSKLIFENVSEHDYNTCVASNKLGHNTA 307
 DB 241 VPSAEFQWYKDDRLIEGKKGVKVENRPLSKLIFENVSEHDYNTCVATNKLGHNTA 300
 QY 308 IMLFPGAVSEVNSGTSRRAG--CVMLLPLVLHLILKF 344
 DB 301 IILYGPAGVHDSGNAASRAAAGLCIM--ATLLARLLILDF 337

RESULT 11
 ID 0723W6 PRELIMINARY; PRT; 338 AA.
 AC 0723W6;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein DKFZp686H1949.
 GN Name=DKFZp686H1949;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human amygdala;
 RA Wamburt R., Heubner D., Mewes H.W., Weill B., Amid C., Oanger A.,
 RA Fodo G., Han M., Wiemann S.,
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX537377; CAD97619.1; -
 DR HSSP; Q9UQH9; I11L.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003598; IG_C2.
 DR Pfam; PF00047; IG_2.
 DR SMART; SM00408; IGc2. 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 KM Hypothetical protein.
 SQ SEQUENCE 338 AA; 37267 MW; EDD86EE2C57B09E3 CRC64;

Query Match 71.7%; Score 1295.5; DB 2; Length 338;
 Best Local Similarity 71.6%; Pred. No. 6e-95;
 Matches 242; Conservative 38; Mismatches 57; Indels 1; Gaps 1;

QY 8 MHNSISMAIFGTALCLFPGVPRSGDATPPKAMDNVTVRQGESATLRTCTIDRVRVA 67
 DB 1 MYHPACIVFETATALLFIFGVPRSGDATPPKAMDNVTVRQGESATLRTCTIDRVRVA 60

DB 1 MYHPACIVFETATALLFIFGVPRSGDATPPKAMDNVTVRQGESATLRTCTIDRVRVA 60
 QY 68 WLRSTLLVAGNDKWCIDPRVLLSNTQYSIEIQNVVDYDEGPYCSVQTDNHPKTSR 127
 DB 61 WLRSTLLVAGNDKWSIDNRVLLSNTKQYSIKIHNVVDYDEGPYCSVQTDNHPKTSR 120
 QY 128 VHLIVQSPKIVEISSDISINEGNNISLTCTIATGRPEPTVTHRISPKAVFVSEDEYLE 186
 DB 121 VHLIVQSPQIVTSSDITVNEGSSVTLMLCLAFGRPEPTVTHRLSGKGFVSEDEYLE 180
 QY 187 EIGITREOSGDYECASNDVAAPVVRKYTVNTPYISAKGTGVPVGOKTLOCEAS 246
 DB 181 EIDITREOSGEYECASNDVAAPVVRKYTVNTPYISAKGTGVPVGOKTLOCEAS 240
 QY 247 AVPSAEFQWYKDDRLIEGKKGVKVENRPLSKLIFENVSEHDYNTCVASNKLGHNTA 306
 DB 241 AVPSAEFQWYKDDRLIEGKKGVKVENRPLSKLIFENVSEHDYNTCVATNKLGHNTA 300
 QY 307 SIMLFPGAVSEVNSGTSRRAGCVMLLPLVLHLILKF 344
 DB 301 SITLYGPAGVHDSGNAASRAAAGLCIM--ATLLARLLILDF 338

RESULT 12
 ID 06GM08 PRELIMINARY; PRT; 345 AA.
 AC 06GM08;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE MGC84065 protein.
 GN Name=MGC84065;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,
 RA Krzyzanski M.I., Skala U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.,
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT Initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;


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DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig_c2.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00409; Ig_3.
DR SMART: SM00408; IgC2; 3.
DR PROSITE: PSS0835; IG_LIKE; 3.
DR SEQUENCE 344 AA; 37868 MW; 15BFE574797B15F3 CRC64;

Query Match 70.3%; Score 1270.5; DB 2; Length 344;
Best Local Similarity 71.1%; Pred. No. 6e-93;
Matches 239; Conservative 37; Mismatches 57; Indels 3; Gaps 1;

QY 12 ISNAITGLAALCLF---QGVPRSGDATFPKAMDNTVROGSSATLRCTIDNRVAV 68
DB 9 LPMKCLVAVSLRLFLVPTGVPRSGDATFPKAMDNTVROGSSATLRCTIDNRVAV 68
QY 69 LNSTSTLYAGNDKWCIDPRVVLSTNTOYSIEIONVDYDEGPTCSVQTDNHPKTSRV 128
DB 69 LNSTSTLYAGNDKWSIDPRVYLIVNTPTQYSIMIONVDYDEGPTCSVQTDNHPKTSRV 128
QY 129 HLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPRAGVSEDEYLEI 188
DB 129 HLIVQVPPQIMNISSDITVNEGSSVTLICAIIGSEPTVTRHISVAGGFVSEDEYLEI 188
QY 189 OGITREGSDGYECSSANDVAAPVRRVKTVPYPISEAKGTGVPVGKGTLCQCEASAV 248
DB 189 SDIKRDSGEYECSSALNDVAAPVRAKVKITVNPYPYISKAKNTGVSQKGIILSCASAV 248
QY 249 PSAEFQWYKDDKRLIEGKGVENRPFSLKIFNVSEHDYGNTCVANLKGHTNASI 308
DB 249 PMAEFQWFKETRIATLDGRILNKGKRMSTLTFNVSEKDYGYNTCVATNKLGTNASI 308
QY 309 MLFPGAVSEVSNCTSRACGVMLLPLVLHLLKLF 344
DB 309 TLVGPAGVIDGVNSASRALACLMLSGTLLAHFFIKF 344

RESULT 15
OPCM HUMAN STANDARD; PRT; 345 AA.
ID OPCM HUMAN
AC 014982;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Opioid binding protein/cell adhesion molecule precursor (OBAM)
DE Opioid-binding cell adhesion molecule (OPCML).
DE Name=OPCML; Synonyms=OBAM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Occipital cortex;
RX MEDLINE=95237612; PubMed=7721093; DOI=10.1016/0378-1119(94)00830-L;
RA Shark K.B., Lee N.M.;
RT "Cloning, sequencing and localization to chromosome 11 of a cDNA
RT encoding a human opioid-binding cell adhesion molecule (OBAM).";
RL Gene 155:213-217(1995)
CC -1- FUNCTION: Binds opioids in the presence of acidic lipids; probably
CC involved in cell contact.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (by
CC similarity).
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. IgION
CC family.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -----
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CC -----
DR EMBL: L34774; AAA36387.1; -.
DR PIR: JC4025; JC4025.
DR Genew: HGNC:8143; OPCML.
DR MIM: 600632; -.
DR GO: GO:0005887; C: integral to plasma membrane; TAS.
DR GO: GO:0004985; F: opioid receptor activity; TAS.
DR GO: GO:0007155; P: cell adhesion; TAS.
DR GO: GO:0008038; P: neuronal cell recognition; TAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig_c2.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00408; IgC2; 2.
DR PROSITE: PSS0835; IG_LIKE; 3.
KW Cell adhesion; Glycoprotein; GPI-anchor; Immunoglobulin domain;
KW Lipoprotein; Repeat; Signal.
FT SIGNAL 1
FT CHAIN 28
FT PROPEP 323
FT DOMAIN 39
FT DOMAIN 136
FT DOMAIN 223
FT DISULFID 57
FT DISULFID 157
FT DISULFID 244
FT CARBOHYD 44
FT CARBOHYD 70
FT CARBOHYD 140
FT CARBOHYD 285
FT CARBOHYD 293
FT CARBOHYD 306
FT LIPID 322
SQ SEQUENCE 345 AA; 38007 MW; E7AD17BEA1A33FF4 CRC64;

Query Match 70.2%; Score 1268; DB 1; Length 345;
Best Local Similarity 71.2%; Pred. No. 9.5e-93;
Matches 240; Conservative 37; Mismatches 56; Indels 4; Gaps 2;

QY 12 ISNAITGLAALCLF---QGVPRSGDATFPKAMDNTVROGSSATLRCTIDNRVAV 68
DB 9 LPMKCLVAVSLRLFLVPTGVPRSGDATFPKAMDNTVROGSSATLRCTIDNRVAV 68
QY 69 LNSTSTLYAGNDKWCIDPRVVLSTNTOYSIEIONVDYDEGPTCSVQTDNHPKTSRV 128
DB 69 LNSTSTLYAGNDKWSIDPRVYLIVNTPTQYSIMIONVDYDEGPTCSVQTDNHPKTSRV 128
QY 129 HLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPK-avgVSEDEYLE 187
DB 129 HLIVQVPPQIMNISSDITVNEGSSVTLICAIIGSEPTVTRHISVAGGFVSEDEYLE 188
QY 188 OGITREGSDGYECSSANDVAAPVRRVKTVPYPISEAKGTGVPVGKGTLCQCEASA 247
DB 188 ISDIKRDQGEYECSSALNDVAAPVRAKVKITVNPYPYISKAKNTGVSQKGIILSCASA 248
QY 248 VPSAEFQWYKDDKRLIEGKGVENRPFSLKIFNVSEHDYGNTCVANLKGHTNASI 307
DB 248 VPMAEFQWFKETRIATLDGRILNKGKRMSTLTFNVSEKDYGYNTCVATNKLGTNASI 308
QY 308 MLFPGAVSEVSNCTSRACGVMLLPLVLHLLKLF 344
DB 309 TLVGPAGVIDGVNSASRALACLMLSGTLLAHFFIKF 345

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Search completed: June 3, 2005, 14:42:06
Job time : 212 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 14:22:01 ; Search time 25 Seconds

(without alignments)
1323.943 Million cell updates/sec

Title: US-09-978-544a-523

Perfect score: 1806

Sequence: 1 MKTIQPMHNSISWIFTL.....RRAGCVLPLVLHLTKF 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

1: PIR.79.*

2: PIR1.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1639.5	90.8	344	2	1F6551
2	1285.5	71.2	338	2	UC1238
3	1268	70.1	345	2	JC4025
4	1266	70.1	345	2	SC0139
5	1259	69.7	345	2	UC1239
6	936.5	51.9	338	2	JC5519
7	931.5	51.6	338	2	UC4776
8	297.5	16.5	333	2	A31923
9	283.5	15.7	725	1	IUMSNG
10	279.5	15.5	725	2	JF0099
11	279.5	15.5	1091	1	IUCHNL
12	278.5	15.4	4162	2	T42633
13	278.5	15.4	858	1	IURINC
14	277.5	15.4	1088	1	IXLNL
15	276	15.3	761	1	IUBONG
16	275.5	15.3	853	1	IUBONG
17	273.5	15.1	725	2	JF0100
18	272.5	15.1	1323	2	PN0568
19	270.5	15.0	1092	1	UN0635
20	261.5	14.5	1091	2	SO1998
21	259	14.3	7962	2	I38346
22	254.5	14.1	5175	2	T20992
23	254.5	14.1	5198	2	T43290
24	249.5	13.8	1040	2	A49356
25	246.5	13.6	1018	2	A54744
26	243.5	13.5	1021	2	A57112
27	243.5	13.5	1036	2	S22383
28	241.5	13.4	1018	2	JC4211
29	241.5	13.4	1018	2	JC4211

30	241.5	13.4	1020	2	S05944	neuronal cell surf
31	240	13.3	3707	2	S18252	heparan sulfate pr
32	235	13.0	662	2	T16525	hypothetical prote
33	234.5	13.0	1040	2	A34695	axonal glycoprotei
34	232.5	12.9	2783	2	T34416	hypothetical prote
35	230.5	12.8	868	2	A46512	CD22 homolog/B lym
36	227.5	12.6	1051	2	A39712	kinase-like protei
37	226	12.5	6642	2	T29757	protein UNC-89 - C
38	225	12.5	4391	2	A38096	perlecan precursor
39	221.5	12.3	862	2	I49583	differentiation an
40	221	12.2	1896	2	T08851	Down syndrome cell
41	220.5	12.2	898	2	A40114	fasciclin II precu
42	219	12.1	1091	2	A58532	glial cell membran
43	218.5	12.1	1612	2	T30805	ducti protein - mo
44	215.5	11.9	1239	1	A32579	neurogliin - fruit
45	214.5	11.9	1070	2	JC4593	protein-tyrosine k
46	214.5	11.9	1651	2	T14160	transmembrane rece
47	214	11.8	495	2	T25750	hypothetical prote
48	211.5	11.7	811	2	A41054	fasciclin II, tran
49	211.5	11.7	871	2	A41054	protein-tyrosine k
50	211.5	11.7	873	2	B41054	fasciclin II PI-11
51	211.5	11.7	891	1	I48697	protein-tyrosine k
52	208.5	11.5	1028	2	A53449	plasmacytoma-assoc
53	205.5	11.3	1028	2	I58164	Big-1 protein - ra
54	204	11.3	1443	2	I50600	neogenin - chicken
55	202	11.2	1273	2	T42405	sax-3 protein - Ca
56	201	11.1	946	1	A47299	ror-related recept
57	199	11.0	1241	2	T37190	nephritn - human
58	199	11.0	847	2	JH0371	B-cell adhesion pr
59	197.5	10.9	1447	2	A54100	tumor suppressor p
60	197	10.9	423	2	T29549	hypothetical prote
61	196	10.9	1906	1	S68235	myosin-light-chain
62	195	10.8	1272	2	S26180	neurofascin - chic
63	195	10.8	1375	2	T13822	frazzed gene prot
64	195	10.8	1526	2	T13823	frazzed gene prot
65	194.5	10.8	1277	2	T30532	neuronal cell adhesi
66	193	10.7	2029	1	TDFPJK	protein-tyrosine-p
67	192.5	10.7	1209	2	T42718	probable neural ce
68	192.5	10.7	1260	1	S05479	neuronal cell adhesi
69	192.5	10.7	1268	1	A39640	neuronal cell adhesi
70	192	10.6	1256	2	T03096	CD0 protein - rat
71	189.5	10.5	765	2	C42632	cell adhesion mole
72	189.5	10.5	812	2	B42632	cell adhesion mole
73	189.5	10.5	932	2	A42632	cell adhesion mole
74	188.5	10.4	1265	1	A37967	neuronal cell adhesi
75	187.5	10.4	1259	2	S36126	hypothetical prote
76	186.5	10.3	1173	2	T25853	CD0 protein - huma
77	186.5	10.3	1240	2	T03097	advanced glycosyla
78	185.5	10.3	404	1	I61596	carcinoembryonic a
79	185.5	10.3	702	2	A36319	rig-1 protein - mo
80	185	10.2	1344	2	T14316	tumor suppressor -
81	185	10.2	1427	1	I51669	myelin-associated
82	184	10.2	582	1	BNRT3S	myelin-associated
83	184	10.2	626	1	S19247	cell adhesion prot
84	184	10.2	1033	2	T43027	neuronal cell adhesi
85	183	10.1	1328	2	T23007	hypothetical prote
86	183	10.1	875	2	T33434	hypothetical prote
87	182.5	10.1	1336	2	I60598	F1C-1 tyrosine kin
88	182.5	10.1	1336	2	I60598	myelin-associated
89	182	10.1	626	1	A61084	neuronal cell adhesi
90	181.5	10.0	1197	2	T30581	receptor tyrosine
91	181.5	10.0	1333	2	I78875	myelin-associated
92	179	9.9	637	2	B33785	telencephalin prec
93	179	9.9	917	2	I48950	hypothetical prote
94	178.5	9.9	483	2	T17346	Bravo/Nr-CAM cell
95	178	9.9	1259	2	A43425	fibroblast growth
96	177.5	9.8	797	2	S38579	hypothetical prote
97	177	9.8	1015	2	T32186	KIAA0992 protein -
98	176.5	9.8	772	2	T13078	hypothetical prote
99	176	9.7	964	2	T15746	hypothetical prote
100	174	9.6	3375	2	T19821	projectin - fruit
101	174	9.6	6658	2	T13931	titin, cardiac mus
102	174	9.6	26926	1	I38344	

103	173.5	9.6	1021	2	T42634	connectin/titin -
104	172.5	9.6	264	2	T26976	hypothetical prote
105	172.5	9.6	976	2	T29583	hypothetical prote
106	172.5	9.6	1880	2	T18531	tracin - medicina
107	172	9.5	286	2	A28333	carcinoembryonic a
108	172	9.5	647	2	A35648	B-cell adhesion pr
109	171.5	9.5	1338	2	S09982	protein-tyrosine k
110	171	9.5	464	2	C30127	transmembrane carc
111	171	9.5	566	1	A32164	billary glycoprote
112	171	9.5	1257	1	A41060	neural cell adhesi
113	170	9.4	812	1	A36477	fibroblast growth
114	169	9.4	764	2	A49448	irregular chiasm C
115	169	9.4	814	1	A39752	fibroblast growth
116	168	9.3	1330	2	S49010	embryonic receptor
117	168	9.3	2051	2	T30938	receptor tyrosine
118	168	9.3	2295	2	C88369	protein unc-52 [im
119	167.5	9.3	523	2	T50478	neurotin - goldfis
120	167.5	9.3	1694	2	S50065	galacthesin - mou
121	167	9.2	816	2	A49151	fibroblast growth
122	167	9.2	822	1	TVMSFG	fibroblast growth
123	167	9.2	1356	2	JC1402	protein-tyrosine k
124	165.5	9.2	538	2	JC2457	vascular cell adhe
125	165.5	9.2	646	2	T38049	cell surface glyco
126	165	9.1	584	2	T08678	hypothetical prote
127	165	9.1	149289	2	T49289	fibroblast growth
128	165	9.1	822	2	S29840	fibroblast growth
129	165	9.1	2222	2	T13924	sekl protein - frui
130	164.5	9.1	583	2	JH03428	alcam - human
131	164.5	9.1	832	2	JH0393	fibroblast growth
132	164	9.1	628	2	T38000	lutheran blood gro
133	163	9.0	818	2	T19120	hypothetical prote
134	162.5	9.0	1535	2	S46224	peroxidasin - frui
135	162	9.0	321	2	JH0395	billary glycoprote
136	162	9.0	351	2	JH0396	billary glycoprote
137	162	9.0	417	2	JH0394	billary glycoprote
138	161	8.9	588	2	T37202	B-CAM protein - hu
139	161	8.9	2341	2	T29340	hypothetical prote
140	160.5	8.9	980	1	TVCTMD	macrophage colony-
141	160	8.9	662	2	C40862	heparin-binding gr
142	160	8.9	822	1	TVHUG	fibroblast growth
143	160	8.9	1437	2	T31093	probable protein-t
144	160	8.9	6831	2	A88852	protein unc-22 [im
145	160	8.9	6839	2	S57242	twitchin [bimilari
146	158.5	8.8	1199	2	T23005	hypothetical prote
147	158	8.7	351	2	PN0020	fibroblast growth
148	158	8.7	822	2	B54846	fibroblast growth
149	157.5	8.7	941	1	TVVMMD	protein-tyrosine k
150	157	8.7	299	1	S56749	junctional adhesio
151	156.5	8.7	416	1	A42879	advanced glycosyla
152	156	8.6	978	2	S16385	macrophage colony-
153	156	8.6	7160	2	T27935	hypothetical prote
154	155.5	8.6	880	2	B53743	protein-tyrosine k
155	155.5	8.6	1138	2	S24673	myosin-binding pro
156	155	8.6	458	1	WMMSR1	billary glycoprote
157	155	8.6	450	2	JC1509	billary glycoprote
158	155	8.6	521	2	JC1508	billary glycoprote
159	155	8.6	521	2	S34338	billary glycoprote
160	155	8.6	1363	2	I58375	protein-tyrosine k
161	155	8.6	1367	2	A41328	protein-tyrosine k
162	154.5	8.6	602	2	A45769	acetylcholine rece
163	154.5	8.6	1897	1	TDHDK	leukocyte antigen-
164	154	8.5	1348	2	S51656	vascular endotheli
165	153.5	8.5	588	2	A45254	surface glycoprote
166	153	8.5	1912	2	A56178	protein-tyrosine-p
167	152.5	8.4	267	2	A38442	probable tumor sup
168	152.5	8.4	458	2	S23969	cell-adhesion mole
169	152	8.4	525	1	A58674	neurotrophin-3 rec
170	152	8.4	803	1	S35695	neurotrophin-3 rec
171	152	8.4	819	1	TVCHFG	fibroblast growth
172	152	8.4	880	1	JC4166	protein-tyrosine k
173	152	8.4	1123	2	S36846	myosin-binding pro
174	151.5	8.4	344	2	A27681	nonspecific cross-
175	151.5	8.4	422	2	S32357	glial growth facto

176	151	8.4	976	1	TVMSMD	macrophage colony-
177	151	8.4	1287	2	T30988	hypothetical prote
178	150.5	8.3	349	2	A34815	carcinoembryonic a
179	150.5	8.3	824	2	S24108	protein-tyrosine k
180	150.5	8.3	1298	2	A48999	protein-tyrosine k
181	150	8.3	769	2	S16236	fibroblast growth
182	150	8.3	822	2	A45081	fibroblast growth
183	150	8.3	822	2	A41794	keratinocyte growt
184	149.5	8.3	739	2	JS0675	vascular cell adhe
185	149.5	8.3	1501	2	I58148	protein-tyrosine-p
186	149.5	8.3	1863	2	S46217	protein-tyrosine-p
187	149	8.3	335	2	H43354	pregnancy-specific
188	149	8.3	1894	2	C54689	protein-tyrosine-p
189	148.5	8.2	587	2	JH0464	DM-GASP precursor
190	148.5	8.2	588	2	JH0506	adhesion molecule
191	148.5	8.2	1907	2	S50893	protein-tyrosine-p
192	147.5	8.2	876	2	T49152	protein-tyrosine k
193	147.5	8.2	1499	2	T50212	protein-tyrosine-p
194	147	8.1	402	2	T09062	probable advanced
195	147	8.1	406	2	B43354	pregnancy-specific
196	146.5	8.1	773	2	T46283	hypothetical prote
197	146	8.1	428	2	A27658	pregnancy-specific
198	146	8.1	852	2	I51259	tyrosine kinase C
199	146	8.1	1088	1	PRRGA	platelet-derived g
200	146	8.1	1089	1	S33727	platelet-derived g
201	145.5	8.1	739	2	JN0581	vascular cell adhe
202	145.5	8.1	799	2	S18209	fibroblast growth
203	145.5	8.1	1898	2	S46216	leukocyte antigen-
204	145	8.0	972	1	TVHMD	macrophage colony-
205	144.5	8.0	1262	1	B48758	protein-tyrosine-p
206	144.5	8.0	1496	1	A48758	protein-tyrosine-p
207	143.5	7.9	1177	2	T16594	hypothetical prote
208	143.5	7.9	13055	2	T16580	Schwann cell myel
209	143	7.9	620	2	JH0593	soluble vascular e
210	143	7.9	687	2	A49636	neuromuscular - fr
211	143	7.9	1011	2	T13669	pregnancy-specific
212	142.5	7.9	326	2	F43354	pregnancy-specific
213	142.5	7.9	435	2	D33258	vascular cell adhe
214	142.5	7.9	739	2	A41288	protein-tyrosine k
215	142	7.8	806	2	A35963	pregnancy-specific
216	141.5	7.8	324	2	A43354	pregnancy-specific
217	141.5	7.8	333	2	A43354	hypothetical prote
218	141.5	7.8	789	2	T28714	hypothetical prote
219	141.5	7.8	1227	2	T23004	hypothetical prote
220	141.5	7.8	1355	2	T28715	fibroblast growth
221	141	7.8	254	2	C42691	fibroblast growth
222	141	7.8	821	1	TVHUF2	fibroblast growth
223	140.5	7.8	397	2	C43354	pregnancy-specific
224	140.5	7.8	705	2	S51635	fibroblast growth
225	140.5	7.8	823	2	B35363	protein-tyrosine k
226	140.5	7.8	1089	1	PFHUGA	platelet-derived g
227	140	7.8	800	1	TVH02F	heparin-binding gr
228	140	7.8	800	2	A48991	fibroblast growth
229	140	7.8	801	2	I55363	fibroblast growth
230	140	7.8	880	1	A53743	protein-tyrosine k
231	140	7.8	976	1	TVHUKT	protein-tyrosine k
232	139.5	7.7	395	2	D43354	pregnancy-specific
233	139.5	7.7	417	2	A28277	pregnancy-specific
234	139.5	7.7	419	2	A33258	pregnancy-specific
235	139.5	7.7	419	2	A31135	pregnancy-specific
236	139.5	7.7	426	2	A35964	pregnancy-specific
237	139.5	7.7	821	1	TVMSBK	fibroblast growth
238	139.5	7.7	1052	2	B49120	protein-tyrosine k
239	139	7.7	824	2	S36439	fibroblast growth
240	139	7.7	987	2	A88746	protein C18P3.2 [i
241	139	7.7	3488	2	T34418	hypothetical prote
242	138.5	7.7	413	2	S65948	hemolin - cestropia
243	138.5	7.7	426	2	B33258	pregnancy-specific
244	138.5	7.7	426	2	A35341	pregnancy-specific
245	138	7.6	1087	2	I51552	platelet-derived g
246	137.5	7.6	419	2	B54312	pregnancy-specific
247	137.5	7.6	882	2	I38912	receptor tyrosine
248	137.5	7.6	1379	2	JC4954	vascular endotheli

249	137	7.6	282	2	C28928	pregnancy-specific	322	124	6.9	436	2	B5181	pregnancy-specific
250	137	7.6	424	2	B36109	pregnancy-specific	323	124	6.9	495	2	A5181	pregnancy-specific
251	137	7.6	458	2	S68177	C-CANMA Protein is	324	124	6.9	650	1	JC1450	fibroblast growth
252	137	7.6	519	2	A44783	ecto-ATPase precu	325	124	6.9	999	2	I38547	novel cellular pro
253	137	7.6	524	2	S35341	ketin - fruit fly	326	124	6.9	1666	2	A48594	skelatin - mouse
254	136.5	7.6	738	2	A40096	platelet-endothel	327	123.5	6.8	402	2	A54312	pregnancy-specific
255	136.5	7.6	822	2	S19947	fibroblast growth	328	123.5	6.8	640	2	A43273	heregulin precursor
256	135.5	7.5	822	2	B49151	fibroblast growth	329	123	6.8	351	2	B34595	pregnancy-specific
257	135.5	7.5	975	2	TC0816	macrophage colony-	330	123	6.8	476	1	A35104	brain-derived neur
258	134.5	7.4	419	2	JC4123	pregnancy-specific	331	123	6.8	821	1	S06943	brain-derived neur
259	134.5	7.4	428	2	I57486	pregnancy-specific	332	123	6.8	1176	2	UN0583	myosin-light-chain
260	134.5	7.4	428	2	US0032	pregnancy-specific	333	122.5	6.8	230	2	A56210	neu differentiatio
261	134.5	7.4	480	2	A56182	fibroblast growth	334	122.5	6.8	241	2	D43273	heregulin precursor
262	134.5	7.4	647	2	B41288	vascular cell adhe	335	122.5	6.8	462	2	I38404	neu differentiatio
263	134.5	7.4	729	2	A49120	fibroblast growth	336	122.5	6.8	636	2	I61718	neu differentiatio
264	134	7.4	238	2	T22098	hypothetical prote	337	122.5	6.8	637	2	C43273	heregulin precursor
265	134	7.4	424	2	A34595	pregnancy-specific	338	122.5	6.8	639	2	I61719	neu differentiatio
266	134	7.4	1147	2	A59307	myosin-light-chain	339	122.5	6.8	645	2	B43273	heregulin, splice
267	133.5	7.4	888	2	S23065	uto protein - mous	340	122.5	6.8	662	2	I61722	neu differentiatio
268	133	7.4	336	2	C27658	pregnancy-specific	341	122	6.8	272	2	I48268	neu differentiatio
269	133	7.4	413	2	A37778	hemolin precursor	342	122	6.8	850	2	JC5700	heregulin precursor
270	133	7.4	473	2	D88976	protein F54E2.4 [i	343	121.5	6.7	332	2	UN0067	pregnancy-specific
271	133	7.4	612	2	I73633	gene tRKC protein	344	121.5	6.7	365	2	UC7780	coxackie- and ade
272	133	7.4	818	2	JC4058	fibroblast growth	345	121.5	6.7	474	1	C39667	brain-derived neur
273	133	7.4	825	2	A55178	neurotrophin recep	346	121.5	6.7	476	1	B39667	brain-derived neur
274	133	7.4	839	2	I73632	neurotrophin-3 rec	347	121.5	6.7	520	1	S44099	brain-derived neur
275	132.5	7.3	273	2	B28928	pregnancy-specific	348	121.5	6.7	818	1	S44098	brain-derived neur
276	132.5	7.3	275	2	A28928	pregnancy-specific	349	121.5	6.7	821	1	A39667	brain-derived neur
277	132.5	7.3	584	2	I50419	pregnancy-specific	350	121.5	6.7	1450	2	A44027	16SK myofibrillar
278	132.5	7.3	856	2	I58411	g-glycerin precursor	351	121	6.7	292	2	T44044	glycoprotein [limpo
279	132	7.3	1048	2	TC0815	platelet-derived g	352	121	6.7	733	2	I49293	fibroblast growth
280	131.5	7.3	480	2	B56182	fibroblast growth	353	121	6.7	994	2	I49276	c-mex tyrosine kin
281	131.5	7.3	499	2	A38429	keratinocyte growt	354	121	6.7	1142	2	C33258	myosin-binding pro
282	131	7.3	499	2	S33766	platelet-derived g	355	120.5	6.7	212	2	C33258	pregnancy-specific
283	131	7.3	811	2	PN0669	connectin I - chic	356	120.5	6.7	353	2	S51242	heparin-binding fi
284	131	7.3	1106	1	PFH068	platelet-derived g	357	120.5	6.7	1742	2	S24600	projectin - fruit
285	130.5	7.2	310	2	JC0119	Fc gamma (IgG) rec	358	119.5	6.6	729	2	A56795	novel antigen rece
286	130.5	7.2	323	2	S06946	Fc gamma (IgG) rec	359	119.5	6.6	684	2	S60261	novel antigen rece
287	130	7.2	802	1	TYH0P4	fibroblast growth	360	119.5	6.6	6805	2	S20926	ritin - rabbit (fir
288	129.5	7.2	419	2	A36109	pregnancy-specific	361	119	6.6	707	2	JC7763	neuronal leucine-r
289	129.5	7.2	707	2	A54846	fibroblast growth	362	119	6.6	820	2	S17295	fibroblast growth
290	129.5	7.2	1040	2	A57638	receptor tyrosine	363	119	6.6	860	2	JC5702	ErbB kinase activa
291	129.5	7.2	1103	2	T22889	hypothetical prote	364	119	6.6	868	2	JC5701	ErbB kinase activa
292	129	7.1	392	1	RWH0P4	poliovirus recepto	365	118	6.5	1274	2	S55050	cardiac myosin-din
293	129	7.1	417	1	RWH0P4	poliovirus recepto	366	118	6.5	1451	2	S42167	190K protein - hum
294	129	7.1	1096	1	PFMSRB	platelet-derived g	367	117.5	6.5	182	2	I83053	pregnancy-specific
295	128.5	7.1	682	1	A35969	heparin-binding gr	368	117.5	6.5	335	2	A33514	pregnancy-specific
296	128	7.1	806	1	TYH0P3	fibroblast growth	369	117.5	6.5	569	2	A36187	interleukin-1 rece
297	127.5	7.1	241	2	S32359	glial growth facto	370	117.5	6.5	978	1	A49814	protein-tyrosine k
298	127	7.0	992	2	A39931	protein-tyrosine k	371	117	6.5	621	2	B57431	myosin-binding C-p
299	126.5	7.0	592	2	S25705	protein-tyrosine k	372	117	6.5	825	1	A40026	neurotrophin-3 rec
300	126.5	7.0	790	2	A39627	protein-tyrosine k	373	117	6.5	894	1	A41527	protein-tyrosine k
301	126	7.0	477	1	I75631	brain-derived neur	374	116.5	6.5	243	2	A37982	calcium vector pro
302	126	7.0	822	1	A56853	brain-derived neur	375	116.5	6.5	282	2	T17129	hypothetical prote
303	126	7.0	940	2	A40985	projectin - fruit	376	116.5	6.5	317	2	JC0118	Fc gamma (IgG) rec
304	126	7.0	1000	2	S18827	Flt3 protein - mou	377	116.5	6.5	599	2	T16774	hypothetical prote
305	125.5	6.9	251	2	T15495	hypothetical prote	378	116	6.4	253	2	T15475	hypothetical prote
306	125.5	6.9	278	2	UC1507	biliary glycoprote	379	116	6.4	268	2	T23555	hypothetical prote
307	125.5	6.9	335	2	B33251	nonspecific cross-	380	116	6.4	330	2	I46691	CO66 precursor - r
308	125.5	6.9	341	2	UC1511	biliary glycoprote	381	116	6.4	416	2	A54017	protein-carcinoma-as
309	125.5	6.9	341	2	UC4024	poliovirus recepto	382	116	6.4	993	2	A36873	protein-tyrosine k
310	125.5	6.9	526	2	S70587	butyrophilin precu	383	115.5	6.4	526	2	A37821	butyrophilin - bov
311	125.5	6.9	975	2	TYMSKT	protein-tyrosine k	384	115.5	6.4	942	2	S23251	protein-tyrosine k
312	125	6.9	278	1	UC1506	biliary glycoprote	385	115	6.4	166	2	A33402	pregnancy-specific
313	125	6.9	341	2	UC1512	biliary glycoprote	386	115	6.4	813	1	A49123	fibroblast growth
314	125	6.9	977	2	I45877	protein-tyrosine k	387	115	6.4	1462	1	B36182	protein-tyrosine-p
315	124.5	6.9	750	2	S41051	fibroblast growth	388	114.5	6.3	326	2	JC4124	pregnancy-specific
316	124.5	6.9	829	2	JC4583	fibroblast growth	389	114	6.3	302	2	C36464	fibroblast growth
317	124.5	6.9	960	1	JN0677	protein-tyrosine k	390	114	6.3	432	1	RW0074	T-cell surface gly
318	124	6.9	278	2	A39037	carcinoembryonic k	391	114	6.3	947	1	I50128	fibroblast growth
319	124	6.9	426	2	C55181	pregnancy-specific	392	114	6.3	947	1	B44294	unc-5 protein, lon
320	124	6.9	426	2	S09016	pregnancy-specific	393	114	6.3	1132	2	A35089	myosin-binding pro
321	124	6.9	426	2	B35334	pregnancy-specific	394	113.5	6.3	344	2	A41357	Fc gamma (IgG) rec

395	113.5	6.3	374	1	A39878
396	113.5	6.3	347	1	S28904
397	113.5	6.3	1465	2	S43529
398	113	6.3	530	2	A53437
399	112.5	6.2	304	1	RMCHT7
400	112.5	6.2	503	2	JC5287
401	112.5	6.2	666	2	H89581
402	112.5	6.2	954	2	I51703
403	112.5	6.2	2109	2	H89066
404	112.5	6.2	2109	2	T33247
405	112	6.2	573	2	S12838
406	112	6.2	1327	2	T09402
407	111.5	6.2	335	2	CS4312
408	111.5	6.2	332	2	B44194
409	111.5	6.2	417	2	A44194
410	111.5	6.2	567	2	S29498
411	111	6.1	210	2	JC4122
412	111	6.1	292	2	T44230
413	111	6.1	398	2	S17428
414	111	6.1	748	2	S41050
415	110.5	6.1	509	2	JC5288
416	110.5	6.1	513	2	S36903
417	110	6.1	285	2	S36903
418	110	6.1	508	2	A33378
419	110	6.1	919	2	T32541
420	110	6.1	1579	2	B91250
421	110	6.1	1700	2	G86131
422	109.5	6.1	164	2	T19795
423	109.5	6.1	196	2	T19794
424	109.5	6.1	206	2	A40305
425	109.5	6.1	470	2	S22080
426	109.5	6.1	532	1	A29849
427	108	6.0	267	2	A56190
428	108	6.0	207	2	I72882
429	108	6.0	474	1	OMHUB
430	108	6.0	464	1	HLMSP3
431	107.5	6.0	352	2	I77374
432	107.5	6.0	404	2	A46460
433	107.5	6.0	537	2	A46611
434	106.5	5.9	336	2	S42632
435	106.5	5.9	367	1	MHCH
436	106	5.9	407	2	T08750
437	105.5	5.8	326	2	T37450
438	105.5	5.8	487	2	T28804
439	105	5.8	131	2	T20334
440	105	5.8	269	2	A46506
441	104.5	5.8	290	2	F42527
442	104	5.8	1471	2	T19506
443	103.5	5.7	240	2	JC4121
444	103.5	5.7	326	1	MWVZ15
445	103.5	5.7	487	2	S65133
446	103.5	5.7	531	2	S20900
447	103.5	5.7	538	2	I68093
448	103	5.7	618	2	T08685
449	103	5.7	943	2	B45082
450	102.5	5.7	257	2	S00682
451	102.5	5.7	336	2	I48471
452	102.5	5.7	1021	2	I39207
453	102	5.6	351	1	SAVZV
454	102	5.6	478	2	I53960
455	102	5.6	1398	2	T25568
456	101.5	5.6	275	2	JC7604
457	101.5	5.6	329	1	A48754
458	101.5	5.6	625	2	T16777
459	101.5	5.6	937	2	A45082
460	101	5.6	351	1	SAVZV
461	101	5.6	353	1	SAVZV
462	101	5.6	421	2	T46266
463	101	5.6	458	1	RWHU74
464	101	5.6	751	2	I48748
465	100.5	5.6	274	2	A47639
466	100	5.5	235	2	S20000
467	100	5.5	304	2	B88746

468	100	5.5	395	2	T05906
469	100	5.5	531	2	S06016
470	100	5.5	537	2	I49769
471	100	5.5	641	2	D71170
472	99	5.5	537	2	A45815
473	99	5.5	1869	2	T44440
474	99	5.5	1160	2	H88369
475	98.5	5.5	629	2	A46500
476	98	5.4	238	2	A49633
477	98	5.4	524	2	J00683
478	98	5.4	544	2	JC5018
479	98	5.4	773	1	ORRBG
480	98	5.4	1000	2	I46521
481	97.5	5.4	197	2	P00327
482	97.5	5.4	270	2	S65739
483	97	5.4	172	2	B26414
484	97	5.4	465	2	B97235
485	97	5.4	874	2	T29548
486	96.5	5.3	309	2	I49503
487	96.5	5.3	364	2	T46926
488	96.5	5.3	437	2	A64488
489	96.5	5.3	475	2	I76668
490	96.5	5.3	580	2	A46538
491	96.5	5.3	709	2	A35364
492	96	5.3	455	1	MHMS
493	96	5.3	455	2	A24576
494	96	5.3	476	1	MHMSM
495	96	5.3	562	2	G02426
496	96	5.3	790	1	TVHUT7
497	95.5	5.3	309	2	S15674
498	95.5	5.3	330	2	A29915
499	95.5	5.3	345	2	A46052
500	95.5	5.3	375	2	I60125
501	95	5.3	267	2	A35902
502	95	5.3	277	2	I52825
503	95	5.3	282	2	S50031
504	95	5.3	329	2	A44065
505	95	5.3	799	1	TVRTTB
506	95	5.3	3283	2	AC1018
507	94.5	5.2	182	2	A34647
508	94.5	5.2	355	2	D72174
509	94.5	5.2	1184	2	T09484
510	94.5	5.2	1280	2	AB1981
511	94.5	5.2	1452	1	S17670
512	94.5	5.2	2347	1	TVHORS
513	94	5.2	338	2	I47159
514	94	5.2	757	2	I45956
515	93.5	5.2	194	2	T29925
516	93.5	5.2	255	2	A55811
517	93.5	5.2	354	2	S46877
518	93.5	5.2	384	2	T28616
519	93.5	5.2	1366	2	B84924
520	93	5.1	144	2	B40098
521	93	5.1	267	2	I56110
522	93	5.1	299	2	I46690
523	93	5.1	352	2	T33433
524	93	5.1	333	2	S16844
525	92.5	5.1	213	2	JE0247
526	92.5	5.1	274	2	T32736
527	92.5	5.1	298	2	H64247
528	92.5	5.1	590	2	T56526
529	92	5.1	1220	2	T32916
530	92	5.1	328	2	I47160
531	92	5.1	460	2	JC2194
532	92	5.1	545	2	TJ00341
533	91.5	5.1	455	2	H96797
534	91	5.0	132	2	S14077
535	91	5.0	370	2	A96741
536	91	5.0	416	2	S33473
537	91	5.0	427	2	G02034
538	90.5	5.0	391	2	T09058
539	90.5	5.0	1269	2	P90538
540	90	5.0	283	1	FCMSG1

probable polygalac
intercellular adhe
intercellular adhe
intercellular adhe
hypothetical prote
intercellular adhe
chitinase (BC 3.2.
protein unc-52 (im
Ly-9.2 antigen - m
Ig lambda-like cha
type-specific anti
intercellular adhe
secretory compon
titin - rabbit (fr
heparin-binding f
basigin precursor
95K nonpeptidic cr
deacetylase/dipep
hypothetical prote
hypothetical prote
B-lymphocyte activ
hypothetical prote
hypothetical prote
pregnancy-specific
Ig heavy chain, se
carcinoembryonic a
Ig mu chain C regi
Ig mu chain C regi
Ig mu chain C regi
interleukin-1 rece
nerve growth facto
cell surface glyco
teratocarcinoma gl
vascular cell adhe
PDGF receptor beta
Fc gamma (IgG) rec
gene MAC25 protein
prostatecyclin-stimu
fibroblast growth
nerve growth facto
large repetitive p
pregnancy-specific
D9R protein - vari
cartilage intermed
hypothetical prote
protein-tyrosine-p
kinase-related pro
Ig gamma 2a chain
polymeric immunogl
hypothetical prote
carcinoembryonic a
B20R protein - var
hypothetical prote
hypothetical prote
colorectal cancer
CD80 precursor - r
hypothetical prote
titin - rabbit (fr
Ig lambda chain NI
hypothetical prote
translation elonga
interleukin 1 rece
hypothetical prote
Ig gamma 2b chain
vasoactive intesti
intercellular adhe
hypothetical prote
hypothetical prote
Ig kappa chain - A
hypothetical prote
interleukin-1 rece
killer cell inhibi
butyrophilin homol
hypothetical prote
Fc gamma (IgG) rec

541	90	5.0	296	2	146021	614	85	4.7	1526	2	T19473	hypothetical prote
542	90	5.0	432	1	RWCZT4	615	85	4.7	2274	2	T30258	adenomatous polyo
543	90	5.0	444	2	G01924	616	85	4.7	2339	2	SA1121	acetyl-CoA carboxy
544	90	5.0	576	2	A32604	617	85	4.7	4351	2	T00252	MGEF1 protein - ra
545	90	5.0	721	2	C82939	618	84.5	4.7	240	2	S01259	OR-45 membrane gly
546	90	5.0	858	1	VCLJ52	619	84.5	4.7	243	2	A53244	leukocyte antigen
547	90	5.0	1357	2	T29265	620	84.5	4.7	330	2	A49601	Fc gamma (IgG) rec
548	90	5.0	1282	2	T42717	621	84.5	4.7	330	2	149660	Fc-gamma-1/gamma-2
549	90	5.0	131	2	F45893	622	84.5	4.7	385	2	T01332	hypothetical prote
550	89.5	5.0	245	2	A30154	623	84.5	4.7	466	2	AP0172	asparagine-tRNA 11
551	89.5	5.0	254	1	UJ0107	624	84.5	4.7	727	2	BS4512	hypothetical prote
552	89.5	5.0	1134	1	A56745	625	84.5	4.7	897	2	BS65127	probable bifunctio
553	89.5	5.0	1134	1	UN0711	626	84.5	4.7	1133	2	T01757	hypothetical prote
554	89.5	5.0	1691	1	D54689	627	84.5	4.7	1227	2	T48028	hypothetical prote
555	89	4.9	257	2	PS0401	628	84	4.7	136	1	KVM521	Ig kappa chain pre
556	89	4.9	271	2	S43512	629	84	4.7	162	2	151668	tumor suppressor -
557	89	4.9	273	2	UX0107	630	84	4.7	225	2	G89936	conserved hypothec
558	89	4.9	275	2	PS0402	631	84	4.7	240	2	UJ0143	antigen BCM1 precu
559	89	4.9	429	1	EHRT	632	84	4.7	246	2	A29523	T-cell surface gly
560	89	4.9	598	2	A57249	633	84	4.7	337	2	AG0963	hypothetical prote
561	89	4.9	769	1	QRRTGS	634	84	4.7	466	2	UC5897	killer cell inhibi
562	89	4.9	1452	1	S17669	635	84	4.7	495	2	UC2195	vasoactive intesti
563	88.5	4.9	309	2	I49522	636	84	4.7	737	2	I39547	S-protein secretio
564	88	4.9	331	2	T15587	637	84	4.7	997	2	D75012	hypothetical prote
565	88	4.9	757	1	S48841	638	84	4.7	1442	2	S72441	protein-tyrosine-p
566	88	4.9	832	2	AD1096	639	84	4.7	1477	2	A43855	high-molecular-wei
567	88	4.9	4436	2	E71086	640	84	4.7	1536	2	A43855	high-molecular-wei
568	87.5	4.8	151	2	T31607	641	83.5	4.6	110	2	B30583	T-cell receptor de
569	87.5	4.8	280	2	I55577	642	83.5	4.6	134	2	S21917	Ig kappa chain V r
570	87.5	4.8	321	2	154766	643	83.5	4.6	245	2	T07071	beta-fructofuranos
571	87.5	4.8	368	2	S17980	644	83.5	4.6	315	1	HNW24X	hemagglutinin prec
572	87.5	4.8	402	2	T29703	645	83.5	4.6	328	2	S30444	SR2 protein - huma
573	87.5	4.8	660	2	H71376	646	83.5	4.6	374	2	S69339	Ig heavy chain V r
574	87	4.8	359	2	A97175	647	83.5	4.6	405	1	B42606	cytochrome P450 CV
575	87	4.8	383	2	T21946	648	83.5	4.6	490	2	B96952	sucrase-6-phosphat
576	87	4.8	814	2	BS4115	649	83.5	4.6	513	2	F86320	hypothetical prote
577	87	4.8	814	2	140048	650	83.5	4.6	583	2	S57721	cpb protein - Clo
578	87	4.8	974	1	A49714	651	83.5	4.6	1054	2	T18304	acid trehalase hom
579	87	4.8	2458	1	T17420	652	83.5	4.6	1657	2	T25421	hypothetical prote
580	86.5	4.8	235	2	S25058	653	83	4.6	220	2	A49444	Ig gamma-1 heavy c
581	86.5	4.8	278	1	TDRTOX	654	83	4.6	313	2	QJ01862	3JR protein - vari
582	86.5	4.8	440	2	D71715	655	83	4.6	315	1	HNW2V	hemagglutinin prec
583	86.5	4.8	1533	2	T00344	656	83	4.6	410	2	C69197	ATP-dependent 26S
584	86	4.8	387	2	T04320	657	83	4.6	555	2	J01526	interleukin-1 rece
585	86	4.8	387	2	T07591	658	83	4.6	563	2	C95874	conserved hypothec
586	86	4.8	444	2	G01925	659	83	4.6	633	2	AE2312	transketolase (mp
587	86	4.8	501	1	A60005	660	83	4.6	680	2	UC5895	killer cell inhibi
588	86	4.8	501	1	VGEBWA	661	83	4.6	767	2	S41479	DNA-binding protei
589	86	4.8	501	1	VGEBWA	662	83	4.6	1014	2	T24412	hypothetical prote
590	86	4.8	505	1	VGEBWA	663	83	4.6	1033	2	A12359	hypothetical prote
591	86	4.8	580	2	A96683	664	83	4.6	2638	1	A42545	genome polyprotein
592	86	4.8	587	2	S36231	665	83	4.6	4836	2	T14346	herc2 protein - mo
593	86	4.8	856	1	A44963	666	82.5	4.6	125	2	A53627	fibroblast growth
594	86	4.8	1394	1	S60762	667	82.5	4.6	150	2	147163	cytoytic trigger
595	86	4.8	1711	2	AB1283	668	82.5	4.6	197	2	S29593	Ig kappa chain (IM
596	85.5	4.7	475	2	A54879	669	82.5	4.6	233	2	UC5322	p53 specific singl
597	85.5	4.7	510	2	PC4054	670	82.5	4.6	247	1	PMWST2	T-cell surface gly
598	85.5	4.7	593	1	DTCMPH	671	82.5	4.6	315	2	T37438	hemagglutinin - va
599	85.5	4.7	764	1	ORHUS	672	82.5	4.6	429	2	T36088	probable secreted
600	85.5	4.7	1145	1	GNTLJEV	673	82.5	4.6	433	2	S31436	Ig upslon chain -
601	85.5	4.7	1146	1	GNTLJ22	674	82.5	4.6	610	2	T25262	hypothetical prote
602	85.5	4.7	1146	1	GNTLJEM	675	82.5	4.6	871	2	H81430	translation initia
603	85.5	4.7	1732	2	T30836	676	82.5	4.6	1553	2	T18502	hypothetical prote
604	85	4.7	505	2	B84831	677	82	4.5	120	2	D29775	Ig kappa chain pre
605	85	4.7	635	2	UC5896	678	82	4.5	225	2	151335	Ig lambda chain -
606	85	4.7	753	2	B36268	679	82	4.5	230	2	S49449	Ig lambda chain -
607	85	4.7	778	2	A60798	680	82	4.5	270	2	A34636	Fc-gamma receptor
608	85	4.7	788	2	I77349	681	82	4.5	288	2	A45803	B-cell-restricted
609	85	4.7	788	2	A26547	682	82	4.5	313	2	H36854	hemagglutinin - va
610	85	4.7	817	2	A48721	683	82	4.5	318	2	F72171	K9R protein - vari
611	85	4.7	832	2	E71452	684	82	4.5	489	1	VGEBTA	glycoprotein A - t
612	85	4.7	939	2	I41197	685	82	4.5	523	1	A60408	glycoprotein SP57-
613	85	4.7	1436	2	UC5290	686	82	4.5	630	2	T38637	hypothetical prote

687	82	4.5	663	1	QRECI	colicin I receptor	760	79.5	4.4	290	2	C97533	pyruvate dehydroge
688	82	4.5	820	2	J14879	hypothetical prote	761	79.5	4.4	306	2	AE2752	pyruvate dehydroge
689	82	4.5	841	2	TC5894	killer cell inhibi	762	79.5	4.4	468	1	AE1242	interleukin-6 rece
690	82	4.5	842	2	T04555	hypothetical prote	763	79.5	4.4	474	2	I50830	Ig mu chain - Lepi
691	82	4.5	1125	1	S57946	protein-tyrosine k	764	79.5	4.4	522	2	B42804	immunodominant typ
692	82	4.5	1222	2	T22490	hypothetical prote	765	79.5	4.4	558	2	A44964	apical membrane an
693	82	4.5	1577	2	PL2058	glucosyltransferas	766	79.5	4.4	653	2	A49722	endoglin precursor
694	81.5	4.5	107	2	PL0268	Ig kappa chain V r	767	79.5	4.4	766	1	CDH026	dipeptidyl-peptida
695	81.5	4.5	240	2	A41797	Ig light chain - s	768	79.5	4.4	1022	1	S00503	Na+/K+-exchanging
696	81.5	4.5	247	2	A34954	T-cell surface gly	769	79.5	4.4	1034	1	A53663	enteropeptidase (E
697	81.5	4.5	259	2	TC7109	SM2V protein - hum	770	79.5	4.4	1036	2	B69368	hypothetical prote
698	81.5	4.5	656	2	TC2338	hypothetical prote	771	79.5	4.4	1156	2	T23308	hypothetical prote
699	81.5	4.5	1183	2	A89135	protein F25G6.2 [1	772	79.5	4.4	1185	2	A42404	collagen adhesin -
700	81.5	4.5	1203	2	S27545	pullulanase - Ther	773	79.5	4.4	1409	2	T42522	protein-tyrosine-P
701	81.5	4.5	1336	2	T17479	hypothetical prote	774	79.5	4.4	1422	2	T30111	hypothetical prote
702	81.5	4.5	1983	2	G86643	hypothetical prote	775	79	4.4	91	2	S17638	Ig kappa chain V r
703	81	4.5	234	2	S14237	Ig kappa chain pre	776	79	4.4	101	2	H37262	Ig heavy chain V r
704	81	4.5	247	2	A55717	myelin/oligodendro	777	79	4.4	231	2	S25753	Ig lambda chain -
705	81	4.5	314	1	HNW2VW	hemagglutinin prec	778	79	4.4	348	2	CB1284	cystathionine beta
706	81	4.5	314	1	J01793	hemagglutinin prec	779	79	4.4	370	2	G97001	endoglucanase fam1
707	81	4.5	451	2	S71754	cellular hepatitis	780	79	4.4	387	2	T04322	polygalacturonase
708	81	4.5	545	2	A38447	oligopeptide ABC t	781	79	4.4	403	2	T20727	hypothetical prote
709	81	4.5	568	2	A45804	Ig mu chain C regi	782	79	4.4	432	2	S30193	T-cell surface gly
710	81	4.5	571	2	H69584	acetylactate synth	783	79	4.4	450	2	B97292	probable ATP-depen
711	81	4.5	578	2	B96683	hypothetical prote	784	79	4.4	474	1	G2MS11	Ig gamma-2b chain
712	81	4.5	585	2	A46507	Ig alpha chain - c	785	79	4.4	659	2	G91009	colicin I receptor
713	81	4.5	588	2	C83836	subtilisin-type pr	786	79	4.4	753	2	G02173	semaphorin III fam
714	81	4.5	637	2	B83052	DnaK protein PA476	787	79	4.4	807	2	A71663	DNA gyrase chain B
715	81	4.5	665	2	E86775	ribonuclease [impo	788	79	4.4	875	2	H90371	proteinase [import
716	80.5	4.5	248	1	Q0BE4L	probable glycoprot	789	79	4.4	1175	2	D85089	hypothetical prote
717	80.5	4.5	269	2	B97501	hypothetical prote	790	79	4.4	1204	2	C75015	probable pyrolysin
718	80.5	4.5	273	2	G89856	conserved hypochet	791	79	4.4	1350	2	AF2005	RNA polymerase bet
719	80.5	4.5	277	2	I47162	Ig gamma 4 chain c	792	79	4.4	1439	2	T27110	hypothetical prote
720	80.5	4.5	288	2	T30086	hypothetical prote	793	78.5	4.3	111	2	D37266	Ig kappa chain V r
721	80.5	4.5	337	2	B97076	UDP-glucose 4-epim	794	78.5	4.3	115	2	B46518	Ig Ii chain V regi
722	80.5	4.5	358	2	A99214	SDS-related conse	795	78.5	4.3	140	2	PH1498	Ig heavy chain V r
723	80.5	4.5	459	2	A46254	CD4 precursor - ra	796	78.5	4.3	228	2	S29575	Ig light chain - r
724	80.5	4.5	466	2	AF0616	asparagine-CRNA 11	797	78.5	4.3	290	1	XYRBM	arylamine N-acetyl
725	80.5	4.5	517	2	B87644	4-comarate-CoA 11	798	78.5	4.3	323	2	JC2578	DNA repair protein
726	80.5	4.5	554	2	A91250	probable portal pr	799	78.5	4.3	373	2	TJ0155	pectin lyase (BC 4
727	80.5	4.5	556	2	D84972	ABC transporter AT	800	78.5	4.3	392	2	T03229	enoyl-lacetyl-carrie
728	80.5	4.5	613	2	T41565	hypothetical prote	801	78.5	4.3	434	2	S72430	transcription elon
729	80.5	4.5	881	2	S67026	probable membrane	802	78.5	4.3	434	2	D88305	protein R03D7.4 [1
730	80.5	4.5	1025	2	G81722	polymorphic membra	803	78.5	4.3	553	1	SMEB11	flagellar hook-ass
731	80.5	4.5	1134	2	SS1471	plasmid replicatio	804	78.5	4.3	553	2	AH0640	B-cell antigen CD1
732	80.5	4.5	1339	1	T08312	killer toxin insen	805	78.5	4.3	556	2	A44441	heat shock protein
733	80.5	4.5	1375	2	TJ0345	dextranucrase (EC	806	78.5	4.3	561	2	T45607	ABC transporter at
734	80.5	4.5	1433	2	T30261	chitinase (BC 3.2.	807	78.5	4.3	590	2	A5635	gadd34 protein - 1
735	80.5	4.5	1457	1	A48066	protein-tyrosine-P	808	78.5	4.3	592	2	S54489	phosphoribosylamin
736	80.5	4.5	1538	2	E70874	probable pps8 prot	809	78.5	4.3	605	1	A48665	methylnalonyl-CoA
737	80.5	4.5	4588	2	T28667	dynein beta heavy	810	78.5	4.3	668	2	JQ0773	penicillin-binding
738	80	4.4	104	2	A40862	T-cell receptor al	811	78.5	4.3	693	2	S46417	heat shock protein
739	80	4.4	150	2	A40862	fibroblast growth	812	78.5	4.3	759	2	B90520	ABC transporter at
740	80	4.4	233	2	IS1383	Ig lambda chain -	813	78.5	4.3	783	2	AG3402	polyphosphate kina
741	80	4.4	239	2	G02630	RealphabD - human	814	78.5	4.3	829	2	B87305	Tomb-dependent rec
742	80	4.4	287	2	JH0332	IGA (Fc) receptor,	815	78.5	4.3	934	2	B29638	paraportal crystal
743	80	4.4	313	2	T28598	hypothetical prote	816	78.5	4.3	1019	2	T40813	probable cell divi
744	80	4.4	425	2	JEO086	SH3-domain binding	817	78.5	4.3	1070	2	T34385	hypothetical prote
745	80	4.4	433	1	S48515	adenylouuccinate s	818	78.5	4.3	1217	2	T00270	hypothetical prote
746	80	4.4	454	1	MHHY	Ig mu chain C regi	819	78.5	4.3	1252	2	T31119	mahq protein - Vib
747	80	4.4	466	2	H96991	secreted protein c	820	78.5	4.3	1385	2	A88554	protein C38C10.5a
748	80	4.4	552	2	S44253	probable N3L prote	821	78.5	4.3	1391	2	B88554	protein C38C10.5b
749	80	4.4	642	2	S44542	probable membrane	822	78.5	4.3	1440	2	JC6312	protein-tyrosine-P
750	80	4.4	680	2	PN0510	integrin beta-3 ch	823	78.5	4.3	1687	2	T43144	vitellogenin II pr
751	80	4.4	937	2	T04194	hypothetical prote	824	78.5	4.3	1858	2	B85547	probable RTX fam1
752	80	4.4	995	2	A56599	embryo kinase 5 -	825	78.5	4.3	5291	2	P90696	hypothetical prote
753	80	4.4	1200	2	T48194	hypothetical prote	826	78	4.3	135	2	S62676	hergulin isoform
754	80	4.4	3343	2	T42207	breat cancer susc	827	78	4.3	131	2	PT0178	Ig kappa chain pre
755	79.5	4.4	155	2	A41675	telokin - rabbit	828	78	4.3	132	2	A55410	Ig light chain V r
756	79.5	4.4	204	2	A69197	hypothetical prote	829	78	4.3	137	2	C45893	T-cell receptor al
757	79.5	4.4	250	2	IS5963	lyt-2.1 lymphocyte	830	78	4.3	178	2	G71195	hypothetical prote
758	79.5	4.4	260	2	A34342	IGF Rc receptor al	831	78	4.3	223	2	S29577	Ig light chain - r
759	79.5	4.4	261	2	S29360	FC gamma (IgG) rec	832	78	4.3	255	2	JC7593	SH2 domain-contain

833	78	4.3	301	1	G64491	thioredoxin-disulf	906	76.5	4.2	267	1	RWMS8	T-cell receptor al
834	78	4.3	328	2	I47158	Ig gamma 1 chain c	907	76.5	4.2	299	1	AHRB	Ig alpha chain C r
835	78	4.3	370	1	HLHNA3	MHC class I histoc	908	76.5	4.2	305	2	B75129	thiamin biosynthes
836	78	4.3	413	2	AG3267	amino-acid N-acety	909	76.5	4.2	332	2	D83745	3-oxoacyl-lacetyl-ca
837	78	4.3	460	2	S67174	hypothetical prote	910	76.5	4.2	403	2	S53477	IMP dehydrogenase
838	78	4.3	475	2	T44566	conserved hypotnet	911	76.5	4.2	428	2	AH3536	dihydroliipoamide S
839	78	4.3	481	2	B82217	asparaginyl-tRNA s	912	76.5	4.2	431	2	A86601	hypothetical prote
840	78	4.3	542	2	A84554	hypothetical prote	913	76.5	4.2	431	2	G72022	probable sodium-tr
841	78	4.3	702	2	T21148	hypothetical prote	914	76.5	4.2	457	2	A27449	T-cell surface gly
842	78	4.3	874	2	C84513	Mutator-like trans	915	76.5	4.2	463	2	T14884	hypothetical prote
843	78	4.3	980	2	H90681	probable flagellin	916	76.5	4.2	483	2	A69745	hypothetical prote
844	78	4.3	980	2	D85532	probable structura	917	76.5	4.2	515	2	H86202	hypothetical prote
845	78	4.3	1016	2	H71460	probable outer mem	918	76.5	4.2	528	2	E70035	levanase homolog y
846	78	4.3	1029	2	P96602	hypothetical prote	919	76.5	4.2	528	2	PC4025	intercellular adhe
847	78	4.3	1138	1	S24066	protein-tyrosine k	920	76.5	4.2	547	2	S75904	hypothetical prote
848	78	4.3	1217	2	P97177	alpha-glucosidase	921	76.5	4.2	563	2	T20631	hypothetical prote
849	78	4.3	2185	1	GNNISV	genome polypotein	922	76.5	4.2	572	1	HNNZB3	hemagglutinin-neur
850	78	4.3	2256	2	AD1018	large repetitive p	923	76.5	4.2	573	2	F89719	protein F09B12.1 l
851	78	4.3	4302	2	A38971	polycyclic kidney	924	76.5	4.2	573	2	T20632	hypothetical prote
852	78	4.3	119	2	PH1519	Ig heavy chain V r	925	76.5	4.2	622	2	A36915	fructanase - Bacte
853	77.5	4.3	140	2	A36194	Ig heavy chain V r	926	76.5	4.2	653	2	B90908	conserved hypotnet
854	77.5	4.3	284	2	S75817	hypothetical prote	927	76.5	4.2	656	2	B71280	probable exported
855	77.5	4.3	307	2	C71002	hypothetical prote	928	76.5	4.2	740	2	AD0465	hypothetical prote
856	77.5	4.3	309	2	T15747	hypothetical prote	929	76.5	4.2	749	2	E86774	probable host spec
857	77.5	4.3	315	1	HNWZVT	hemagglutinin prec	930	76.5	4.2	775	2	G90996	hypothetical prote
858	77.5	4.3	428	2	T48167	hypothetical prote	931	76.5	4.2	782	2	A85693	hypothetical prote
859	77.5	4.3	446	2	S40295	Ig gamma-2a chain	932	76.5	4.2	896	2	T22061	valyl-tRNA synthet
860	77.5	4.3	466	2	C85619	asparagine tRNA by	933	76.5	4.2	913	2	E75554	protein F2 - Strept
861	77.5	4.3	466	2	E90755	transcription fact	934	76.5	4.2	1039	2	T30856	protein-tyrosine k
862	77.5	4.3	469	1	TVHUE2	immunodominant typ	935	76.5	4.2	1124	1	I58388	hypothetical prote
863	77.5	4.3	532	2	C42804	phosphonocetaledeh	936	76.5	4.2	1131	2	T14517	hypothetical prote
864	77.5	4.3	534	2	S60205	probable polyketid	937	76.5	4.2	1151	2	S48431	probable membrane
865	77.5	4.3	584	2	T05052	internalin protein	938	76.5	4.2	1248	2	C89874	autolysin [importe
866	77.5	4.3	593	2	A11235	hypothetical prote	939	76.5	4.2	1363	2	C84346	hypothetical prote
867	77.5	4.3	655	2	T34219	probable membrane	940	76.5	4.2	1377	2	I54632	tan protein - Bacch
868	77.5	4.3	668	2	S49639	envelope protein h	941	76.5	4.2	1648	2	S61654	fibronectin precur
869	77.5	4.3	676	2	T30480	env polypeptide pr	942	76.5	4.2	2477	2	S14428	Ig light chain V r
870	77.5	4.3	852	1	VCLJG3	cell differentiat	943	76.5	4.2	91	2	PH1071	Ig kappa chain V r
871	77.5	4.3	888	2	A54280	hypothetical prote	944	76.5	4.2	107	2	PD0011	Ig kappa chain V r
872	77.5	4.3	1192	2	T08609	probable membrane	945	76.5	4.2	108	2	G30560	Ig kappa chain V r
873	77.5	4.3	1474	2	F69009	4-alpha-glucanotra	946	76.5	4.2	108	2	S38720	Ig light chain V r
874	77.5	4.3	1515	2	A40203	uncharacterized pr	947	76.5	4.2	118	2	I33932	Ig kappa chain pre
875	77.5	4.3	1819	2	D97033	protein H19M22.1 l	948	76.5	4.2	120	2	C29775	Ig kappa chain pre
876	77.5	4.3	1825	2	C88400	hypothetical prote	949	76.5	4.2	161	2	S04931	T-cell receptor de
877	77.5	4.3	1825	2	T32828	breast cancer susc	950	76.5	4.2	251	2	S64927	probable membrane
878	77.5	4.3	3329	2	T42205	filamentous hemagg	951	76.5	4.2	254	2	B75052	coenzyme pqg synth
879	77.5	4.3	3329	2	T30904	Ig kappa chain V r	952	76.5	4.2	310	2	F90011	conserved hypotnet
880	77.5	4.3	3591	1	S21010	Ig kappa chain V r	953	76.5	4.2	327	2	T07104	2'-hydroxydihydrod
881	77	4.3	107	2	PC4405	Ig kappa chain V-J	954	76.5	4.2	327	2	S06611	Ig gamma-2 chain C
882	77	4.3	128	2	S40343	hypothetical prote	955	76.5	4.2	365	2	D87526	hypothetical prote
883	77	4.3	234	2	S01330	Ig kappa chain pre	956	76.5	4.2	426	2	H84846	probable polygalac
884	77	4.3	302	2	S50579	hypothetical prote	957	76.5	4.2	430	2	T28143	tepasin 1 homolog,
885	77	4.3	328	2	I47161	Ig gamma 3 chain c	958	76.5	4.2	431	2	F71476	probable sodium-tr
886	77	4.3	338	2	S09276	Ig alpha chain C r	959	76.5	4.2	450	1	MHDG	Ig mu chain C regi
887	77	4.3	384	2	B84871	probable polygalac	960	76.5	4.2	473	2	H83676	pyruvate dehydrog
888	77	4.3	439	2	AE1251	probable peptidogl	961	76.5	4.2	501	2	E96509	protein P27F5.17 l
889	77	4.3	614	2	A88466	protein B0244.2 li	962	76.5	4.2	505	1	ACRYG1	nicotinic acetylch
890	77	4.3	817	2	P86742	ribonuclease [impo	963	76.5	4.2	511	2	E84685	probable seed stor
891	77	4.3	859	2	AC2089	adenylate cyclase	964	76.5	4.2	516	2	A44494	cAMP-responsive el
892	77	4.3	879	2	C90879	hypothetical prote	965	76.5	4.2	577	2	T48530	clathrin binding p
893	77	4.3	879	2	G85739	hypothetical prote	966	76.5	4.2	656	2	AC0429	2',3'-cyclic-nucle
894	77	4.3	928	2	A87749	protein F55C7.7c l	967	76.5	4.2	859	1	VCLJCT	env polypeptide pr
895	77	4.3	976	2	C96958	ACT domain contain	968	76.5	4.2	1020	2	A46405	C protein alpha an
896	77	4.3	1071	1	PXBIVV	H+-exporting ATPas	969	76.5	4.2	1151	2	S03722	DNA-directed DNA p
897	77	4.3	1176	2	A33856	surface-layer 125K	970	76.5	4.2	1176	2	H86389	hypothetical prote
898	77	4.3	2488	2	T42739	guanine nucleotide	971	76.5	4.2	1298	2	A47462	probable DNA-direc
899	77	4.3	3562	2	A47171	chondroitin sulfat	972	76.5	4.2	1366	2	S57664	IGA-specific metal
900	76.5	4.2	135	2	PH1492	Ig heavy chain V r	973	76.5	4.2	2380	2	T29551	hypothetical prote
901	76.5	4.2	136	2	A49137	Ig kappa chain pre	974	75.5	4.2	104	2	JC6076	anti-D-dimer monoc
902	76.5	4.2	178	2	S29594	Ig kappa chain (WM	975	75.5	4.2	114	2	S44119	Ig kappa chain V-J
903	76.5	4.2	232	2	S17399	Ig lambda chain pr	976	75.5	4.2	123	2	S35479	Ig kappa chain pre
904	76.5	4.2	236	2	A24637	T-cell surface gly	977	75.5	4.2	131	2	S09259	Ig kappa chain pre
905	76.5	4.2	252	2	AF2719	arginine-tRNA-prot	978	75.5	4.2	131	2	D29380	Ig kappa chain pre

979	75.5	4.2	132	2	PH0106	anti-digoxin trans	1052	75	4.2	1311	2	T33757	hypothetical prote
980	75.5	4.2	133	2	S40324	Ig kappa chain V r	1053	75	4.2	1313	2	GC2887	hypothetical prote
981	75.5	4.2	140	1	HVMSG7	Ig heavy chain pre	1054	75	4.2	1476	2	AC2220	hypothetical prote
982	75.5	4.2	140	2	PH1489	Ig heavy chain V r	1055	75	4.2	1661	2	H71439	hypothetical prote
983	75.5	4.2	189	2	T39849	anaphase promoting	1056	75	4.2	1672	2	T46237	hypothetical prote
984	75.5	4.2	231	2	PC4155	Ig gamma-2b chain	1057	75	4.2	2291	2	S11238	polymerase - Berne
985	75.5	4.2	234	2	A39956	Ig lambda chain pr	1058	75	4.2	2413	2	S34570	splicing factor PR
986	75.5	4.2	248	2	F96655	hypothetical prote	1059	75	4.2	2500	2	G71609	hypothetical prote
987	75.5	4.2	249	2	C69081	acetyl-CoA synthet	1060	74.5	4.1	116	1	HVMS1B	Ig heavy chain pre
988	75.5	4.2	252	2	T42986	v-cyclin - ateline	1061	74.5	4.1	119	2	PH1517	Ig heavy chain V r
989	75.5	4.2	316	2	RB6157	hypothetical prote	1062	74.5	4.1	119	2	PH1516	Ig heavy chain V r
990	75.5	4.2	341	2	S72445	DNA-binding protei	1063	74.5	4.1	140	2	PH1488	Ig heavy chain V r
991	75.5	4.2	362	2	S16303	polysialacturonase	1064	74.5	4.1	192	2	T02893	hypothetical prote
992	75.5	4.2	362	2	T46475	hypothetical prote	1065	74.5	4.1	232	2	S25756	Ig lambda chain -
993	75.5	4.2	402	2	F70850	DNA-directed DNA p	1066	74.5	4.1	243	2	AC3071	transcription regu
994	75.5	4.2	504	2	S00390	Ig gamma chain (cl	1067	74.5	4.1	277	2	S29922	SalB1L protein pre
995	75.5	4.2	524	2	D87440	2-isopropylmalate	1068	74.5	4.1	300	1	HVRKCS	Ig mu chain C regi
996	75.5	4.2	569	2	A46462	T cell activation	1069	74.5	4.1	397	2	S70987	dnan protein - Msc
997	75.5	4.2	580	2	S49308	beta-fructofuranos	1070	74.5	4.1	438	2	B97712	hypothetical prote
998	75.5	4.2	582	2	S53814	DEAD box protein -	1071	74.5	4.1	466	1	SYBCNT	asparagine-tRNA 11
999	75.5	4.2	641	2	JC7142	dextranase (EC 3.2	1072	74.5	4.1	468	1	P2WL51	L2 protein - human
1000	75.5	4.2	691	1	S46735	NADPH-ferrihemopro	1073	74.5	4.1	501	2	S74341	Ig heavy chain prote
1001	75.5	4.2	710	1	A46273	mitochondrial inte	1074	74.5	4.1	549	2	S04845	L-lactate dehydrog
1002	75.5	4.2	713	1	A1B8G7	cyclomalodextrin	1075	74.5	4.1	591	1	CB8V2	hypothetical prote
1003	75.5	4.2	739	2	A55314	glycine-tRNA ligas	1076	74.5	4.1	644	2	S50552	hypothetical prote
1004	75.5	4.2	746	2	E64701	conserved hypochet	1077	74.5	4.1	663	2	AG0782	collicin I receptor
1005	75.5	4.2	771	2	B70564	hypothetical prote	1078	74.5	4.1	693	2	JN0843	heat shock protein
1006	75.5	4.2	815	2	AB2444	hypothetical prote	1079	74.5	4.1	729	2	T46270	histone transcript
1007	75.5	4.2	857	1	S05943	gelation factor -	1080	74.5	4.1	807	2	T39479	histone transcript
1008	75.5	4.2	918	2	D71407	hypothetical prote	1081	74.5	4.1	862	2	E88594	protein Y48A68.11
1009	75.5	4.2	1068	2	S73091	hypothetical prote	1082	74.5	4.1	899	2	AB3019	conserved hypochet
1010	75.5	4.2	1167	2	A99273	hypothetical prote	1083	74.5	4.1	947	2	T26314	hypothetical prote
1011	75.5	4.2	1818	2	AE3011	conserved hypochet	1084	74.5	4.1	1043	2	D84900	hypothetical prote
1012	75.5	4.2	1871	2	D96698	probable DNA polym	1085	74.5	4.1	1183	2	S63046	probable membrane
1013	75.5	4.2	1894	2	T02155	DNA-directed DNA p	1086	74.5	4.1	1403	2	T11583	probable translati
1014	75.5	4.2	2265	1	FNBO	fibronectin - bovi	1087	74.5	4.1	1622	2	T45240	hypothetical prote
1015	75.5	4.2	5005	2	E82884	hypothetical prote	1088	74.5	4.1	1825	2	S13507	microtubule-associ
1016	75.5	4.2	6669	2	S55024	nebulin, skeletal	1089	74.5	4.1	1830	2	A37981	microtubule-associ
1017	75	4.2	106	2	A49138	IgA kappa rheumato	1090	74.5	4.1	2338	2	T173957	kinase-related pro
1018	75	4.2	115	2	B26524	T-cell receptor be	1091	74.5	4.1	2366	2	S10317	toxin B - Clostrid
1019	75	4.2	117	2	S40362	Ig kappa chain - h	1092	74.5	4.1	2761	2	T21064	hypothetical prote
1020	75	4.2	138	2	A47159	Ig lambda chain V	1093	74.5	4.1	4572	2	S57908	hypothetical 527K
1021	75	4.2	130	2	C29380	Ig kappa chain pre	1094	74.5	4.1	4639	1	A54794	dynein heavy chain
1022	75	4.2	131	2	D34904	Ig kappa chain pre	1095	74	4.1	107	2	S12954	Ig kappa chain V r
1023	75	4.2	148	2	PH0115	Ig heavy chain pre	1096	74	4.1	108	2	T26681	hypothetical prote
1024	75	4.2	157	2	D31327	IgB receptor alpha	1097	74	4.1	131	2	S52449	Ig kappa chain V r
1025	75	4.2	215	2	A57843	sodium channel bet	1098	74	4.1	196	2	S72716	4-commarate-CoA 11
1026	75	4.2	246	2	E69230	hypothetical prote	1099	74	4.1	221	1	Q0BE48	BARF1 protein - hu
1027	75	4.2	268	2	A56446	Ig heavy chain V r	1100	74	4.1	231	2	S25751	Ig lambda chain -
1028	75	4.2	283	2	AH1767	protoporphyriogen	1101	74	4.1	248	2	D45831	MHC class I histoc
1029	75	4.2	285	2	B82842	spermidine synhas	1102	74	4.1	277	2	D42521	MHC class I histoc
1030	75	4.2	297	2	AC2380	hypothetical prote	1103	74	4.1	365	2	I37476	HLA-A30.3 precurs
1031	75	4.2	307	1	RMMSBC	T-cell receptor be	1104	74	4.1	365	2	I56039	MHC class I histoc
1032	75	4.2	321	2	S10006	hypothetical prote	1105	74	4.1	365	2	I38519	MHC class I histoc
1033	75	4.2	359	2	AF3184	beta-lactamase (im	1106	74	4.1	416	1	A41267	transcription fact
1034	75	4.2	364	2	S03535	class I histocompa	1107	74	4.1	429	2	AC1522	flagellar hook-agg
1035	75	4.2	392	2	T34095	zinc finger protei	1108	74	4.1	438	1	HVRKCS	Ig mu chain C regi
1036	75	4.2	393	2	T03216	enoyl-l-facyl-carrie	1109	74	4.1	449	1	B64706	hemolysin - Helico
1037	75	4.2	394	2	G69230	endo-1,4-beta-gluc	1110	74	4.1	454	2	T26296	hypothetical prote
1038	75	4.2	416	2	E64140	hypothetical prote	1111	74	4.1	461	1	HVRKCO	Ig mu chain C regi
1039	75	4.2	435	2	T42613	probable envelope	1112	74	4.1	468	1	TVMSGE2	transcription fact
1040	75	4.2	439	2	G97159	contains cell adhe	1113	74	4.1	474	2	T47299	hypothetical prote
1041	75	4.2	444	2	B90053	hypothetical prote	1114	74	4.1	514	2	G89903	conserved hypochet
1042	75	4.2	476	2	S64291	glycoprotein F - h	1115	74	4.1	523	2	F85489	2-isopropylmalate
1043	75	4.2	479	1	VGBBER2	glycoprotein F - h	1116	74	4.1	523	2	F90638	2-isopropylmalate
1044	75	4.2	535	2	S76564	hypothetical prote	1117	74	4.1	523	2	B64729	hypothetical prote
1045	75	4.2	574	2	T29005	hypothetical prote	1118	74	4.1	552	2	AH2084	2-isopropylmalate
1046	75	4.2	577	2	I50731	Ig heavy chain - n	1119	74	4.1	573	2	T02743	hypothetical prote
1047	75	4.2	701	2	C97910	ATP-dependent prot	1120	74	4.1	579	2	D87063	probable acyl-CoA
1048	75	4.2	733	2	T34853	probable fusidic a	1121	74	4.1	587	2	S63033	hypothetical prote
1049	75	4.2	775	1	J01639	outer layer protei	1122	74	4.1	701	2	C97302	hypothetical prote
1050	75	4.2	780	2	T31548	hypothetical prote	1123	74	4.1	755	2	T48553	subtilisin-like pr
1051	75	4.2	1242	1	DJBBC1	DNA-directed DNA p	1124	74	4.1	876	2	TS1507	MD40-repeat protei

1125	74	4.1	879	2	H64888	membrane protein y	1198	73	4.0	469	2	D95969	conserved hypother
1126	74	4.1	908	2	T25035	hypothetical prote	1199	73	4.0	478	2	S47040	gene Tc52 protein
1127	74	4.1	966	2	B87473	TonB-dependent rec	1200	73	4.0	481	2	C97238	Arg dependent RNA
1128	74	4.1	1085	2	JC2237	probable helicase	1201	73	4.0	523	2	A12696	serine proteinase
1129	74	4.1	1128	2	H90538	hypothetical prote	1202	73	4.0	522	2	A97479	probable serine pr
1130	74	4.1	1132	1	QSBPL	host specificity p	1203	73	4.0	565	2	H69342	GTP-binding protei
1131	74	4.1	1136	1	S57845	protein-cytosine k	1204	73	4.0	586	2	T45945	lactase-like prote
1132	74	4.1	1137	2	B90734	probable host spec	1205	73	4.0	657	2	AD1525	probable cell surf
1133	74	4.1	1482	2	S13495	pregnancy zone pro	1206	73	4.0	671	2	T23015	hypothetical prote
1134	74	4.1	1488	2	C70984	probable ppsB prot	1207	73	4.0	673	2	H86761	glycine-cRNA ligas
1135	74	4.1	1524	2	A96950	DNA segregation AT	1208	73	4.0	673	2	T41768	AcMNPV orf23 - Bom
1136	74	4.1	1963	2	B98002	Iga-specific metal	1209	73	4.0	688	2	S39491	protochlorophyllid
1137	74	4.1	2185	1	GNNVSH	genome polyprotein	1210	73	4.0	701	2	H95039	hypothetical prote
1138	74	4.1	23271	2	T43271	phosphotidylinosit	1211	73	4.0	722	2	D70200	polyribonucleotide
1139	74	4.1	2812	2	S20961	keratinocyte growt	1212	73	4.0	745	2	B33856	hypothetical 80k p
1140	73.5	4.1	96	2	PH1070	Ig light chain V r	1213	73	4.0	754	2	H86592	general secretion
1141	73.5	4.1	97	2	S26341	Ig light chain V r	1214	73	4.0	754	2	D72032	general secretion
1142	73.5	4.1	119	2	PH1510	Ig heavy chain V r	1215	73	4.0	771	2	AE2056	cation transportin
1143	73.5	4.1	119	2	PH1518	Ig heavy chain V r	1216	73	4.0	772	2	A46108	outer capsid prote
1144	73.5	4.1	133	2	PC1155	Ig heavy chain pre	1217	73	4.0	858	2	T12142	lipoxygenase (EC 1
1145	73.5	4.1	135	2	PH1493	Ig heavy chain V r	1218	73	4.0	870	2	T47454	lipoxygenase AtLOX
1146	73.5	4.1	140	2	PH1486	Ig heavy chain V r	1219	73	4.0	896	2	JQ2391	lipoxygenase (EC 1
1147	73.5	4.1	140	2	PH1483	Ig heavy chain V r	1220	73	4.0	897	2	S67283	hypothetical prote
1148	73.5	4.1	229	2	A20969	Ig kappa chain pre	1221	73	4.0	935	2	S66306	hypothetical prote
1149	73.5	4.1	309	2	T09564	glutaminyl-peptide	1222	73	4.0	980	2	T39630	valine-cRNA ligase
1150	73.5	4.1	339	2	T28138	Ig V-region-like B	1223	73	4.0	1095	2	T24061	hypothetical prote
1151	73.5	4.1	340	2	T28137	Ig V-region-like B	1224	73	4.0	1336	2	T18288	ABC transport prot
1152	73.5	4.1	366	2	AF0497	DNA-directed DNA p	1225	73	4.0	1473	2	A35186	salivary agglutini
1153	73.5	4.1	380	2	S12839	Ig heavy chain pre	1226	73	4.0	1518	2	T28880	hypothetical prote
1154	73.5	4.1	388	2	S95007	sugar isomerase do	1227	73	4.0	1815	2	B95942	conserved hypother
1155	73.5	4.1	400	2	T22853	probable cathepsin	1228	73	4.0	2207	2	S09553	genome polyprotein
1156	73.5	4.1	418	2	G87469	ThlJ/BfpI family p	1229	73	4.0	2210	1	RXXPRV	genome polyprotein
1157	73.5	4.1	422	2	A96912	glutamate-1-semial	1230	73	4.0	2907	2	S45728	fibrillin-2 precur
1158	73.5	4.1	431	2	S37775	filamin, muscle -	1231	73	4.0	3011	1	S40770	genome polyprotein
1159	73.5	4.1	505	2	AC3486	cell surface prote	1232	73	4.0	3263	2	B82410	hypothetical prote
1160	73.5	4.1	579	2	B84956	cell division prot	1233	73	4.0	4688	2	F82885	hypothetical prote
1161	73.5	4.1	632	2	C98246	5'-nucleotide adp	1234	73	4.0	4936	2	AH2515	hypothetical prote
1162	73.5	4.1	636	2	AF3020	5'-nucleotide adp	1235	72.5	4.0	124	2	S40364	Ig kappa chain - h
1163	73.5	4.1	677	2	T40145	probable beta-adap	1236	72.5	4.0	126	2	S40312	Ig kappa chain - h
1164	73.5	4.1	725	2	C87485	ComEC/Rec2 family	1237	72.5	4.0	128	2	S20636	Ig kappa chain V r
1165	73.5	4.1	815	2	E70021	3-hydroxyacyl-CoA	1238	72.5	4.0	137	2	E34903	Ig heavy chain pre
1166	73.5	4.1	941	2	S29043	cellulase (BC 3.2.	1239	72.5	4.0	141	2	T14718	Ig heavy chain var
1167	73.5	4.1	986	2	B81675	polymorphic membra	1240	72.5	4.0	198	2	T19797	hypothetical prote
1168	73.5	4.1	1005	2	T18537	Ig heavy chain - c	1241	72.5	4.0	199	2	G75153	hypothetical prote
1169	73.5	4.1	1052	2	H83909	cell wall-associat	1242	72.5	4.0	215	2	T64004	hypothetical prote
1170	73.5	4.1	1119	2	A86340	protein F2D10.24 l	1243	72.5	4.0	219	2	S38855	Ig kappa chain - m
1171	73.5	4.1	1121	2	I38127	phosphoprotein pho	1244	72.5	4.0	233	1	UU0284	fc gamma (19c) rec
1172	73.5	4.1	1280	2	T00365	hypothetical prote	1245	72.5	4.0	247	2	PQ0655	outer capsid spike
1173	73.5	4.1	1285	2	B72420	hypothetical prote	1246	72.5	4.0	247	2	PQ0656	outer capsid spike
1174	73.5	4.1	1292	2	T09229	galactose binding	1247	72.5	4.0	247	2	PQ0657	outer capsid spike
1175	73.5	4.1	1330	1	GQFPE	epidermal growth f	1248	72.5	4.0	264	2	F27579	T-cell receptor al
1176	73.5	4.1	1487	2	S15904	alpha-1 proteinase	1249	72.5	4.0	267	2	PL0064	T-cell receptor be
1177	73.5	4.1	1571	2	T00062	hypothetical prote	1250	72.5	4.0	286	2	S32480	hypothetical prote
1178	73.5	4.1	3328	2	T30835	breast cancer cumo	1251	72.5	4.0	288	2	S29690	Ig heavy chain VDJ
1179	73.5	4.1	126	2	S24704	Ig heavy chain V6	1252	72.5	4.0	289	2	G00031	B7 protein - red-c
1180	73	4.0	127	2	PH1234	Ig kappa chain pre	1253	72.5	4.0	312	2	D82690	adenine-specific m
1181	73	4.0	128	2	PN0445	Ig kappa chain pre	1254	72.5	4.0	322	2	T50167	hypothetical prote
1182	73	4.0	131	2	E25733	T-cell receptor al	1255	72.5	4.0	350	2	T21106	hypothetical prote
1183	73	4.0	132	2	A27632	T-cell receptor al	1256	72.5	4.0	377	2	T05453	trehalose-6-phosph
1184	73	4.0	133	1	K4H0J1	Ig kappa chain pre	1257	72.5	4.0	401	2	B87531	hypothetical prote
1185	73	4.0	145	2	S21651	T-cell receptor be	1258	72.5	4.0	408	2	D95417	probable ABC trans
1186	73	4.0	225	2	B82473	hypothetical prote	1259	72.5	4.0	423	2	F64436	hypothetical prote
1187	73	4.0	233	2	S25747	Ig lambda chain -	1260	72.5	4.0	428	2	B84964	adenosylmethionine
1188	73	4.0	332	2	G83458	sulfate-binding pr	1261	72.5	4.0	451	2	T48340	hypothetical prote
1189	73	4.0	349	2	T08782	hypothetical prote	1262	72.5	4.0	453	2	C31933	Ig mu chain C regi
1190	73	4.0	389	2	B42708	serine-type D-Ala-	1263	72.5	4.0	475	2	S01331	Ig gamma-2b chain
1191	73	4.0	393	1	HVRKC1	Ig mu chain C regi	1264	72.5	4.0	482	2	T49079	serine-type carbox
1192	73	4.0	438	1	HVRKC2	Ig mu chain C regi	1265	72.5	4.0	498	2	G92729	protein containing
1193	73	4.0	445	2	S67695	26S proteasome reg	1266	72.5	4.0	503	2	B72289	oligopeptide ABC t
1194	73	4.0	451	1	S75239	hypothetical prote	1267	72.5	4.0	527	2	T22000	hypothetical prote
1195	73	4.0	454	2	AE1970	hypothetical prote	1268	72.5	4.0	533	2	A42249	aspartic proteinase
1196	73	4.0	469	1	F2WL35	L2 protein - human	1269	72.5	4.0	560	2	B81451	flagellar W-ring p
1197	73	4.0	469	2	S36525	L2 protein - human	1270	72.5	4.0	668	2	T05803	hypothetical prote

1271	72.5	4.0	676	2	F69276	conserved hypochet	1344	72	4.0	992	2	T46337	hypothetical prote
1272	72.5	4.0	736	2	D96830	probable heat-shoc	1345	72	4.0	1076	1	A35622	nuclear pore prote
1273	72.5	4.0	759	1	B60080	RNA-directed RNA p	1346	72	4.0	1083	2	S48460	probable membrane
1274	72.5	4.0	836	2	A69550	hypothetical prote	1347	72	4.0	1106	2	A97647	cation efflux syst
1275	72.5	4.0	887	1	JUCHCL	B-cadherin precurs	1348	72	4.0	1106	2	AG2870	Acr family transp
1276	72.5	4.0	894	2	S61015	hypothetical prote	1349	72	4.0	1132	2	H90834	host specificity p
1277	72.5	4.0	941	2	F97353	uncharacterized co	1350	72	4.0	1149	2	T27567	hypothetical prote
1278	72.5	4.0	954	2	S57108	hypothetical prote	1351	72	4.0	1155	2	H71456	probable pyrolysin
1279	72.5	4.0	970	2	T18842	receptor protein-c	1352	72	4.0	1199	2	S77082	pyruvate (flavodox
1280	72.5	4.0	1039	2	T15885	hypothetical prote	1353	72	4.0	1245	1	VHWB2	structural polypro
1281	72.5	4.0	1166	2	T29009	hypothetical prote	1354	72	4.0	1391	2	S50608	hypothetical prote
1282	72.5	4.0	1186	2	T42729	histocompatibility	1355	72	4.0	1408	2	H69068	cell surface glyco
1283	72.5	4.0	1212	2	T42387	histocompatibility	1356	72	4.0	2094	2	S33124	lpr protein - huma
1284	72.5	4.0	1228	2	G90581	hypothetical prote	1357	72	4.0	2567	2	A49551	filamin, Muller ce
1285	72.5	4.0	1229	2	T25697	hypothetical prote	1358	72	4.0	2902	2	C71953	toxin-like outer m
1286	72.5	4.0	1276	2	B86546	polymorphic outer	1359	72	4.0	3890	2	C89921	hypothetical prote
1287	72.5	4.0	1276	2	C81591	polymorphic membra	1360	72	4.0	246	1	A32999	polyketide synthas
1288	72.5	4.0	1306	2	S22624	aggregation protei	1361	71.5	4.0	91	2	S17628	Ig kappa chain V r
1289	72.5	4.0	1383	2	T13052	guanine nucleotide	1362	71.5	4.0	119	2	PH1503	Ig heavy chain V r
1290	72.5	4.0	1431	2	A45866	dextranucrase (BC	1363	71.5	4.0	121	2	S44113	Ig heavy chain V r
1291	72.5	4.0	1500	1	JQ1348	carbamoyl-phosphat	1364	71.5	4.0	129	2	S40347	Ig kappa chain - h
1292	72.5	4.0	1665	2	T29008	hypothetical prote	1365	71.5	4.0	225	2	JI0029	Ig kappa chain pre
1293	72.5	4.0	1966	2	T08891	hypothetical prote	1366	71.5	4.0	246	1	A32999	myelin P0 protein
1294	72.5	4.0	2004	2	F95133	immunoglobulin A1	1367	71.5	4.0	275	2	H35216	FP31 protein - fow
1295	72.5	4.0	2052	2	C97038	phage-related prot	1368	71.5	4.0	275	2	C82752	hypothetical prote
1296	72.5	4.0	3924	2	S37431	ankyrin 2, neuroma	1369	71.5	4.0	290	2	T40852	cystathionine beta
1297	72.5	4.0	4845	2	T31067	BIR repeat contain	1370	71.5	4.0	303	2	H71693	hypothetical prote
1298	72	4.0	115	1	KVMSK2	Ig kappa chain pre	1371	71.5	4.0	305	2	B84413	probable oligopept
1299	72	4.0	115	1	A30995	T-cell receptor be	1372	71.5	4.0	321	2	F71163	hypothetical prote
1300	72	4.0	131	2	B34904	Ig kappa chain pre	1373	71.5	4.0	325	2	H90269	Ig gamma-2 chain C
1301	72	4.0	131	2	B30577	Ig kappa chain pre	1374	71.5	4.0	326	1	G2HD	homeotic protein C
1302	72	4.0	133	2	T45927	membrane-bound imm	1375	71.5	4.0	340	2	S20879	Ig gamma-2 chain H
1303	72	4.0	148	2	PH0121	Ig heavy chain pre	1376	71.5	4.0	360	2	H95980	probable uroporphyr
1304	72	4.0	148	2	PH0119	Ig heavy chain pre	1377	71.5	4.0	361	2	S78542	dtDPglucose 4,6-de
1305	72	4.0	208	1	WMNV15	18.5K protein - Au	1378	71.5	4.0	384	2	AI2962	cellulose synthesi
1306	72	4.0	223	2	F81795	CTLA-4 precursor -	1379	71.5	4.0	389	2	E98320	hypothetical prote
1307	72	4.0	229	2	F81795	probable periplasm	1380	71.5	4.0	476	2	A46118	myosin-binding pro
1308	72	4.0	338	2	A53066	CCNAF enhancer-bin	1381	71.5	4.0	477	2	UC4386	adenyl cyclase-a
1309	72	4.0	340	2	T02639	G5 protein homolog	1382	71.5	4.0	493	2	S39299	hexon protein - hu
1310	72	4.0	349	2	F70357	lipoprotein - Aqu	1383	71.5	4.0	507	1	A43387	polymerase-associa
1311	72	4.0	351	2	JQ2166	spindle body prote	1384	71.5	4.0	507	2	AC3036	glycerol-3-phospha
1312	72	4.0	372	1	UHHUCN	ciliary neurotroph	1385	71.5	4.0	507	2	H98249	glpD gene homolog
1313	72	4.0	375	2	A64398	hypothetical prote	1386	71.5	4.0	520	2	A13295	adenylosuccinate s
1314	72	4.0	386	2	E84562	probable tub fam11	1387	71.5	4.0	523	1	S48997	IMP dehydrogenase
1315	72	4.0	411	1	VGBEG2	glycoprotein G pre	1388	71.5	4.0	572	2	B46529	Ig y heavy chain (
1316	72	4.0	411	2	A37755	xyylanase (EC 3.2.1	1389	71.5	4.0	592	2	JC4642	purH bifunctional
1317	72	4.0	424	2	H96963	dihydroorotase lim	1390	71.5	4.0	608	2	T32708	hypothetical prote
1318	72	4.0	425	2	AC2959	HlyD family secret	1391	71.5	4.0	611	2	T45493	glutamine-fructose
1319	72	4.0	428	2	T08626	sarcosine reductas	1392	71.5	4.0	647	2	F70057	penicillin-binding
1320	72	4.0	430	2	T32055	hypothetical prote	1393	71.5	4.0	659	2	S36551	BI protein - human
1321	72	4.0	433	2	S76485	hypothetical prote	1394	71.5	4.0	668	2	T44118	penicillin-binding
1322	72	4.0	441	2	AF0048	modification methy	1395	71.5	4.0	668	2	JQ0774	penicillin-binding
1323	72	4.0	452	2	C98324	hypothetical prote	1396	71.5	4.0	751	2	AI1392	phosphoribosylform
1324	72	4.0	454	2	A46532	Ig mu chain C regi	1397	71.5	4.0	775	1	T37422	glutamine-cRNA lig
1325	72	4.0	513	2	D96943	probable polygalac	1398	71.5	4.0	775	2	A32494	transposable eleme
1326	72	4.0	515	2	AH2996	glycerol-3-phospha	1399	71.5	4.0	776	2	S59790	hypothetical prote
1327	72	4.0	531	2	A98287	glpD gene homolog	1400	71.5	4.0	860	2	AC05882	leucyl-tRNA synthet
1328	72	4.0	531	2	T50964	related to RCC1 pr	1401	71.5	4.0	893	2	F86476	protein F1504.39 l
1329	72	4.0	570	2	A57535	intrileukin 1 recep	1402	71.5	4.0	928	2	C97728	hypothetical prote
1330	72	4.0	570	2	A57535	hypothetical prote	1403	71.5	4.0	958	2	S32435	Na+/Ca2+-exchangin
1331	72	4.0	574	2	E64414	hypothetical prote	1404	71.5	4.0	1021	2	T15765	hypothetical prote
1332	72	4.0	576	2	G81657	DNA mismatch repair	1405	71.5	4.0	1025	2	T110259	RNA-directed DNA p
1333	72	4.0	627	2	S14683	Ig mu chain precur	1406	71.5	4.0	1031	2	D88912	protein T06A10.1 l
1334	72	4.0	665	2	F97032	beta-glucosidase f	1407	71.5	4.0	1031	2	T33655	hypothetical prote
1335	72	4.0	697	2	T27587	hypothetical prote	1408	71.5	4.0	1094	2	S22573	DNA-directed DNA p
1336	72	4.0	777	1	TVPVCP	large T antigen -	1409	71.5	4.0	1125	2	H87644	TonB-dependent rec
1337	72	4.0	782	2	S22560	large T antigen -	1410	71.5	4.0	1128	1	T08322	plasmid replicatio
1338	72	4.0	844	2	T37690	hypothetical prote	1411	71.5	4.0	1231	2	S30185	insulin receptor s
1339	72	4.0	844	2	T52396	formin-binding pro	1412	71.5	4.0	1250	2	T40062	probable nuclear e
1340	72	4.0	868	2	D86349	hypothetical prote	1413	71.5	4.0	1441	2	T13717	CRAG protein - fru
1341	72	4.0	878	1	RRX81B	RNA-directed RNA p	1414	71.5	4.0	1446	2	S73013	polyketide synthas
1342	72	4.0	892	2	T06818	DNA topoisomerase	1415	71.5	4.0	1448	2	AI2007	Subtilase family p
1343	72	4.0	984	2	C84781	hypothetical prote	1416	71.5	4.0	1526	2	AC2239	WD-40 repeat prote

1417	71.5	4.0	1540	2	H87203	polyketide synthas
1418	71.5	4.0	1592	2	S63208	hypothetical prote
1419	71.5	4.0	1603	1	VJWXS	vitellogenin vit-5
1420	71.5	4.0	1797	2	P69195	cell surface glyco
1421	71.5	4.0	2013	2	A11469	probable peptidogl
1422	71.5	4.0	2014	2	I36936	complement recepto
1423	71.5	4.0	2767	1	UIHU	thyroglobulin prec
1424	71.5	4.0	3670	2	T36249	CBA peptidic synthe
1425	71.5	4.0	4342	2	H83343	probable non-ribos
1426	71.5	4.0	5105	2	T32650	hypothetical prote
1427	71.5	4.0	6359	2	T31679	bactetracin synthe
1428	71.5	4.0	15281	2	S41309	cyclosporin synthe
1429	71.5	3.9	115	1	K3HUCI	ig kappa chain pre
1430	71.5	3.9	115	2	D27552	T-cell receptor be
1431	71.5	3.9	128	2	T12517	hypothetical prote
1432	71.5	3.9	128	2	S40373	ig kappa chain - h
1433	71.5	3.9	128	2	A56701	ig kappa chain V r
1434	71.5	3.9	128	2	A26406	ig kappa chain V r
1435	71.5	3.9	131	2	B32513	ig kappa chain pre
1436	71.5	3.9	133	2	E82603	hypothetical prote
1437	71.5	3.9	139	2	G32536	T-cell receptor al
1438	71.5	3.9	148	2	PH0116	ig heavy chain pre
1439	71.5	3.9	197	2	T16627	hypothetical prote
1440	71.5	3.9	223	2	T09536	cytotoxic T-lympho
1441	71.5	3.9	224	2	F98215	transcription regu
1442	71.5	3.9	240	2	S06084	ig kappa chain pre
1443	71.5	3.9	255	2	G83543	conserved hypochet
1444	71.5	3.9	261	2	AC0164	probable transport
1445	71.5	3.9	277	2	T37424	probable 31.5K pro
1446	71.5	3.9	313	2	A34677	secretory pathway
1447	71.5	3.9	319	2	B53290	oligopeptide trans
1448	71.5	3.9	323	2	B72224	conserved hypochet
1449	71.5	3.9	336	2	C83926	S-adenosylmethion
1450	71.5	3.9	344	2	A69325	hypothetical prote
1451	71.5	3.9	356	2	T40041	hypothetical prote
1452	71.5	3.9	357	2	E86823	peptidoglycan synt
1453	71.5	3.9	368	2	G81289	UDPgalactopyranose
1454	71.5	3.9	375	2	H86938	conserved hypochet
1455	71.5	3.9	397	2	P66680	PSII1.10 imported
1456	71.5	3.9	400	2	T34363	hypothetical prote
1457	71.5	3.9	404	2	AF2225	hypothetical prote
1458	71.5	3.9	405	1	VGBEGF	glycoprotein G pre
1459	71.5	3.9	429	2	AC1163	flagellar hook-ass
1460	71.5	3.9	431	2	H81738	probable sodium-tr
1461	71.5	3.9	440	2	JL0144	interleukin-6 rece
1462	71.5	3.9	460	2	JL0145	interleukin-6 rece
1463	71.5	3.9	462	2	S74579	carboxyl-terminal
1464	71.5	3.9	472	2	AH3353	serine-type D-Ala-
1465	71.5	3.9	476	2	T19786	hypothetical prote
1466	71.5	3.9	478	2	H86100	hypothetical prote
1467	71.5	3.9	482	2	AC0426	serine-type D-Ala-
1468	71.5	3.9	501	2	T13316	hypothetical prote
1469	71.5	3.9	503	2	T40650	hypothetical prote
1470	71.5	3.9	507	2	JQ1929	phosphoprotein - r
1471	71.5	3.9	516	2	F82070	2-isopropylmalate
1472	71.5	3.9	522	2	E69116	conserved hypochet
1473	71.5	3.9	642	2	G69371	acetyl-CoA synthe
1474	71.5	3.9	646	2	T27899	hypothetical prote
1475	71.5	3.9	659	2	A85854	hypothetical prote
1476	71.5	3.9	660	2	AD0661	lipoasin-like prote
1477	71.5	3.9	695	2	S66662	protein-glutamine
1478	71.5	3.9	784	2	F97981	exoribonuclease R
1479	71.5	3.9	786	2	F95977	protein tyrosine k
1480	71.5	3.9	837	2	S43656	furin (EC 3.4.21.7
1481	71.5	3.9	848	2	T28055	hypothetical prote
1482	71.5	3.9	922	2	T40372	tp asp repeat pro
1483	71.5	3.9	946	1	A29550	methylesterase
1484	71.5	3.9	1015	2	S68141	nuclear protein HI
1485	71.5	3.9	1032	2	T23164	hypothetical prote
1486	71.5	3.9	1035	2	T23165	hypothetical prote
1487	71.5	3.9	1036	2	T05687	beta-galactosidase
1488	71.5	3.9	1057	2	T16676	hypothetical prote
1489	71.5	3.9	1081	2	T15692	hypothetical prote

1490	71	3.9	1144	2	A36968	P1-like adhesin pr
1491	71	3.9	1145	2	T05573	hypothetical prote
1492	71	3.9	1152	2	AC1347	probable peptidogl
1493	71	3.9	1268	2	B99789	hemagglutinin/hemo
1494	71	3.9	1270	2	E85649	hypothetical prote
1495	71	3.9	1341	2	S09579	tail fiber protein
1496	71	3.9	1500	1	SYRTCA	carbamoyl-phosphat
1497	71	3.9	1555	2	S38758	amylo-alpha-1,6-gl
1498	71	3.9	2062	2	G96602	probable receptor
1499	71	3.9	2163	2	S50675	pre-mRNA splicing
1500	71	3.9	2183	2	T42764	coagulation factor

ALIGNMENTS

RESULT 1
 156551
 neurotlimin - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C/Accession: 156551
 R/Struyk, A.F.; Canoll, P.D.; Wolfgang, M.J.; Rosen, C.L.; D'Eustachio, P.; Salzer, J.L.
 J. Neurosci. 15, 2141-2156, 1995
 A/Title: Cloning of neurotlimin defines a new subfamily of differentially expressed neur
 A/Reference number: 156551; PMID:95198094; PMID:7891157
 A/Accession: 156551
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-344 <RES>
 A/Cross-reference: UNIPROT:Q62718; EMBL:U16845; NID:G755184; PIDN:AAA67445.1; PID:G7551;
 C/Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal

Query Match 90.8%; Score 1639.5; DB 2; Length 344;
 Best Local Similarity 92.9%; Pred. No. 2-56-113;
 Matches 312; Conservative 9; Mismatches 12; Indels 3; Gaps 1;

QY	12	ISNAIFGTALALCLF--	OGPVRSGDATPPKAMDNTVVRQGSATLRCTIDNHTVRAM	68
DB	9	LPMKCLVVSRLRLFLVPTGVPVRSAGATPPKAMDNTVVRQGSATLRCTIDNHTVRAM		68
QY	69	LNSTIIYAANDKWCIDPRVLLSNTQYISIEIQNDVYDEGPTCSVQTDNHPKTSRV		128
DB	69	LNSTIIYAANDKWCIDPRVLLSNTQYISIEIQNDVYDEGPTCSVQTDNHPKTSRV		128
QY	129	HLIVQVSPKIVEISSDISINEGNNISITCIATGPREPTVMRHISPRAVGVSDYLEI		188
DB	129	HLIVQVSPKIVEISSDISINEGNNISITCIATGPREPTVMRHISPRAVGVSDYLEI		188
QY	189	OGITREQSGDYECASANDVAPVVRKYVTWNPYISBAKGTVPVGOKGTLCCEASAV		248
DB	189	OGITREQSGDYECASANDVAPVVRKYVTWNPYISBAKGTVPVGOKGTLCCEASAV		248
QY	249	PSAEFQYKDKRLIEBKKGVKVENRPPSLKLIFFNVSEHDYGNITCVASNKLGHYNASI		308
DB	249	PSAEFQYKDKRLIEBKKGVKVENRPPSLKLIFFNVSEHDYGNITCVASNKLGHYNASI		308
QY	309	MLFPGAVSEVSNCTSRACGWLPLVYLHLIKF		344
DB	309	MLFPGAVSEVSNCTSRACGWLPLVYLHLIKF		344

RESULT 2

JCI238
 opioid-binding protein (clone DU21) - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
 C/Accession: JCI238
 R/Lipman, D.A.; Lee, N.M.; Loh, H.H.
 Gene 117, 249-254, 1992
 A/Title: Opioid-binding cell adhesion molecule (OBGAM)-related clones from a rat brain c
 A/Reference number: JCI238; PMID:92347701; PMID:1339369
 A/Accession: JCI238

A:Molecule type: mRNA
 A:Residues: 1-338 <LIP>
 C:Species: UniProt:P32736; GB:M88709; NID:g203245; PID:AAA4085.1; PID:g203246
 A:Experimental source: brain
 C:Genetic: OBCAM
 A:Gene: OBCAM
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

Query Match 71.2%; Score 1285.5; DB 2; Length 338;
 Best Local Similarity 71.6%; Pred. No. 2.8e-87;
 Matches 242; Conservative 35; Mismatches 60; Indels 1; Gaps 1;

QY 8 MNSISWALFTGLAALCLFQGVPRSGDATPPKAMDNVTVROGSATLCTIDNRVTVRA 67
 DB 1 MYHAPYVFSATYALFLFPGVPRSGDATPPKAMDNVTVROGSATLCTIDNRVTVRA 60
 QY 68 WLNRSITLYAGNDKCLDPRVLLSTNTQOYSIEIONVDVYDGPYCSVQTDNHPKTSR 127
 DB 61 WLNRSITLYAGNDKMSIDPRVLLVNTPTQYSIMIQNVVDYDGPYCSVQTDNHPKTSR 120
 QY 128 VHLIVQVSPKIVEISSDISINEGNISLTCIATGRPEPTVTHHSFK-ANGVSEDEYL 186
 DB 121 VHLIVQVPPQIMNISSDITVNEISVTLCLALGRPEPTVTHHLSVKEGQGFVSEDEYL 180
 QY 187 EICGTRBQSGDYECASANDVAPVVRVRYVTVNPPYISBAGTGVPCQKGLTQCEAS 246
 DB 181 EISDIRDQSGEYECASALNDVAPVVRKVKITVNPYISKAKNTGVSVQKGLTQCEAS 240
 QY 247 AVSAEPQWKDRLIEGKKGVKVENRPLSKLIFNVSEHGYNTCVASNKLGHTNA 306
 DB 241 AVMAEQWFKEDTRLATGIDGVRIEKKGRISTLTFNVSEKQYGTCAVTKNLGHTNA 300
 QY 307 SIMLFGGAVSEVNGTSRRAGCWLPLPLVHLHLKLF 344
 DB 301 SITLGGAVVIDGVNSASRALACLMLSGTFPAHFPIKF 338

RESULT 3

JC4025

oploid-binding cell adhesion protein - human

C:Species: Homo sapiens (man)

C>Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 09-Jul-2004

C/Accession: JC4025

R:Shark, K.B.; Lee, N.M.

Gene 155, 213-317, 1995

A>Title: Cloning, sequencing and localization to chromosome 11 of a cDNA encoding a huma

A:Reference number: JC4025; MUID:95237612; PMID:7721093

A/Accession: JC4025

A:Molecule type: mRNA

A:Residues: 1-345 <SHA>

A:Cross-references: UNIPROT:Q14982; GB:J34774; NID:g514373; PID:AAA36387.1; PID:g514374

A:Experimental source: brain

C:Comment: This protein binds oploid alkaloids in the presence of acidic lipids, exhibit

C:Genetic: OBCAM; OBCAM; OPCM

A:Gene: GDB:OPCM; OBCAM; OPCM

A:Cross-references: GDB:251677; OMIM:600632

A/Map position: 11pter-11qter

C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

Query Match 70.2%; Score 1268; DB 2; Length 345;
 Best Local Similarity 71.2%; Pred. No. 5.7e-86;
 Matches 240; Conservative 37; Mismatches 56; Indels 4; Gaps 2;

QY 12 ISWALFTGLAALCLF---QGVPRSGDATPPKAMDNVTVROGSATLCTIDNRVTVRA 68
 DB 9 LPMKCLVVSRLFLVPTGVPRSGDATPPKAMDNVTVROGSATLCTIDNRVTVRA 68
 QY 69 LNRSTLYAGNDKMSIDPRVLLSTNTQOYSIEIONVDVYDGPYCSVQTDNHPKTSR 128
 DB 69 LNRSTLYAGNDKMSIDPRVLLSTNTQOYSIEIONVDVYDGPYCSVQTDNHPKTSR 128
 QY 129 HLIIVQVSPKIVEISSDISINEGNISLTCIATGRPEPTVTHHSFK-ANGVSEDEYL 187
 DB 129 HLIIVQVSPKIVEISSDISINEGNISLTCIATGRPEPTVTHHSFK-ANGVSEDEYL 187

DB 129 HLIIVQVPPQIMNISSDITVNEISVTLCLALGRPEPTVTHHLSVKEGQGFVSEDEYL 188
 QY 188 IQGTRBQSGDYECASANDVAPVVRVRYVTVNPPYISBAGTGVPCQKGLTQCEASA 247
 DB 189 ISDTRDQSGEYECASALNDVAPVVRKVKITVNPYISKAKNTGVSVQKGLTQCEASA 248
 QY 248 VPSAEQWFKEDTRLATGIDGVRIEKKGRISTLTFNVSEKQYGTCAVTKNLGHTNA 307
 DB 249 VPMAEQWFKEDTRLATGIDGVRIEKKGRISTLTFNVSEKQYGTCAVTKNLGHTNA 308

QY 308 IMLFGGAVSEVNGTSRRAGCWLPLPLVHLHLKLF 344
 DB 309 ITLGGAVVIDGVNSASRALACLMLSGTFLPAHFPIKF 345

RESULT 4

S03199

oploid-binding protein OPCAM precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004

C/Accession: S03199

R:Schotfield, P.R.; McFarland, K.C.; Hayflick, J.S.; Wilcox, J.N.; Cho, T.M.; Roy, S.; Lee

EMBO J. 8, 489-495, 1989

A>Title: Molecular characterization of a new immunoglobulin superfamily protein with pote

A:Reference number: S03199; MUID:89251576; PMID:2721489

A/Accession: S03199

A:Molecule type: mRNA

A:Residues: 1-345 <SCH>

A:Cross-references: UNIPROT:P11834; EMBL:X12672; NID:g5985; PID:CAA31192.1; PID:g5986

C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

C:Keywords: Transmembrane protein

F:1-27/Domain: signal sequence #status predicted <SIG>

F:28-345/Product: oploid-binding protein OPCAM #status predicted <MAT>

Query Match 70.1%; Score 1266; DB 2; Length 345;
 Best Local Similarity 71.6%; Pred. No. 8e-86;
 Matches 240; Conservative 34; Mismatches 57; Indels 4; Gaps 2;

QY 14 WALFTGLAALCLF---QGVPRSGDATPPKAMDNVTVROGSATLCTIDNRVTVRA 70
 DB 11 WKCLVVSRLFLVPTGVPRSGDATPPKAMDNVTVROGSATLCTIDNRVTVRA 70
 QY 71 RSTLYAGNDKMSIDPRVLLSTNTQOYSIEIONVDVYDGPYCSVQTDNHPKTSR 130
 DB 71 RSTLYAGNDKMSIDPRVLLSTNTQOYSIEIONVDVYDGPYCSVQTDNHPKTSR 130
 QY 131 IYVQVSPKIVEISSDISINEGNISLTCIATGRPEPTVTHHSFK-ANGVSEDEYL 189
 DB 131 IYVQVPPQIMNISSDITVNEISVTLCLALGRPEPTVTHHLSVKEGQGFVSEDEYL 190
 QY 190 GITRQSGDYECASANDVAPVVRVRYVTVNPPYISBAGTGVPCQKGLTQCEASA 249
 DB 191 DIRDQSGEYECASALNDVAPVVRKVKITVNPYISKAKNTGVSVQKGLTQCEASA 250
 QY 250 SAEQWFKEDTRLATGIDGVRIEKKGRISTLTFNVSEHGYNTCVASNKLGHTNA 309
 DB 251 MAEQWFKEDTRLATGIDGVRIEKKGRISTLTFNVSEKQYGTCAVTKNLGHTNA 310
 QY 310 LFGGAVSEVNGTSRRAGCWLPLPLVHLHLKLF 344
 DB 311 LFGGAVVIDGVNSASRALACLMLSGTFLPAHFPIKF 345

RESULT 5

JC1239

oploid-binding protein (clones S68 and SG13) - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

C/Accession: JC1239

R:Lipman, D.A.; Lee, N.M.; Loh, H.H.

Gene 117, 249-254, 1992

A>Title: Opioid-binding cell adhesion molecule (OBCAM)-related clones from a rat brain cl

A:Reference number: JC1238; MUID:92347701; PMID:1339369

A31923
amaJam protein precursor - fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*
C/Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 09-Jul-2004
C/Accession: A31923
R/Seeger, M.A.; Haffley, L.; Kaufman, T.C.
Cell 55, 589-600, 1988
A/Title: Characterization of amaJam: a member of the immunoglobulin superfamily from *D. A.*
A/Reference number: A31923; MUID:89028670; PMID:3141062
A/Accession: A31923
A/Molecule type: DNA
A/Residues: 1-333 <SRE>
A/Cross-references: UNIPROT:P15364; GB:M23561; NID:g156920; PIDN:AAA28367.1; PID:g156921
C/Genetics:
A/Gene: *FlyBase:Ama*
A/Cross-references: *FlyBase:Fbgn0000071*

Query Match 16.5%; Score 297.5; DB 2; Length 333;
Best Local Similarity 29.7%; Pred. No. 1.5e-14;
Matches 87; Conservative 43; Mismatches 136; Indels 27; Gaps 11;

QY 44 NVTROGESATLCTIDN-RVTRVAMLR-----STIYAGNDKWCIDPR--VLLASN 93
Db DVVASVDSVFNCTVVEVQGLSVMAKRSESDPTNSVLSMRTIISLPDKRNVVTYEG 92

QY 94 TGTQ---YSIEIONVDYDEGPTCSVQTDNHPK-TSRVHLIVQVSPKIVE-ISSDISIN 148
Db 93 PKTGSALYTFRIQNIIEVSDMGPEYQVLVATEKVTKLSIQIKTPPIVAENTPKSTLYT 152

QY 149 EGNINSLTCTATGRPEPTVWRH----ISPKAVFVSEDEYLEIQITRQSGDYESAS 204
Db 153 EGNLELTCTHANGPKPTIISAREHNAVMP-AGHLLAEPTLRISVHRDRGGYYCIAQ 211

QY 205 NDVAAPVRRVRYKVTNPPYIS-EAKGTGVVQCKTGLQCEASAVPAEFQWYKDRLLI 263
Db 212 NGSGQPKRLIRVEVERPQIAVGRPKIAQWHSABLECSVQCYPAPTYVMHNGVPL- 270

QY 264 EGKGVKVENR-----PFLSKLIFENVSEHDYGNVTCVANSKLGHTNASIMLF 311
Db 271 QSSRHHVANTASSSGTTTSVLRIDSVGEEDFGDYCNATNKLGHADARLHLF 323

RESULT 9
IUMSNG
neural cell adhesion molecule 1 precursor, GPI-anchored splice form - mouse
N/Alternate names: NCAM-120
C/Species: *Mus musculus* (house mouse)
C/Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C/Accession: A29673; S00382; A44220
R/Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fontec
EMBO J. 6, 907-914, 1987
A/Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000
A/Reference number: A29673; MUID:87246524; PMID:33595563
A/Accession: A29673
A/Molecule type: mRNA
A/Residues: 1-725 <BAR>
A/Cross-references: UNIPROT:P13594; EMBL:Y00051; NID:G53342; PIDN:CAA68263.1; PID:G53343
R/Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-632, 1988
A/Title: Differential splicing and alternative polyadenylation generates distinct NCAM t
A/Reference number: S00382; MUID:88283628; PMID:3336534
A/Accession: S00382
A/Molecule type: DNA
A/Residues: 642-656, 'D', 658-725 <BA2>
A/Cross-references: EMBL:X07195
R/Rougon, G.; Marchak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A/Title: Structural and immunological characterization of the amino-terminal domain of m
A/Accession: A44290; MUID:86140120; PMID:3512556
A/Molecule type: protein
A/Residues: 20-36 <ROU>
C/Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol

C/Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IUMS
C/Genetics:
A/Gene: NCAM
A/Map position: 9
A/Insertions: 701/1
C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C/Keywords: alternative splicing; cell adhesion; duplication; heparin binding; membrane
F/1-19/Domain: signal sequence #status predicted <Sig>
F/34-98/Domain: immunoglobulin homology <IMM1>
F/132-191/Domain: immunoglobulin homology <IMM2>
F/152-156/Region: heparin binding #status predicted
F/161-165/Region: heparin binding #status predicted
F/228-290/Domain: immunoglobulin homology <IMM3>
F/263-272/Region: NCAM binding #status predicted
F/323-388/Domain: immunoglobulin homology <IMM4>
F/420-482/Domain: immunoglobulin homology <IMM5>
F/519-596/Domain: fibronectin type III repeat homology <FN3A>
F/625-685/Domain: fibronectin type III repeat homology <FN3B>
F/41-96,139-189,235-288,330-386,427-480/Dsulfide bonds: #status predicted
F/222,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.7%; Score 283.5; DB 1; Length 725;
Best Local Similarity 25.8%; Pred. No. 4.4e-13;
Matches 75; Conservative 45; Mismatches 130; Indels 41; Gaps 7;

QY 44 NVTROGESATLCTIDN-RVTRVAMLRSTIYAGNDKWCIDPRV-----LISNTQ 95
Db 222 NATANLQGSVTLVCDADG-----PPEPTM-----SWTKDEPIENEBEDRSRSVS 268

QY 96 TQYISLIONVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNISL 155
Db 269 DSEVTRIRANDKDEAEVYCIENKRAEQDASLHLVFAKPKTYVENGTAMELEQVTL 328

QY 156 TCTATGRPEPTVWR-----HISPKAVFVSEDEYLEIQITRQSGDYE 200
Db 329 TCASQDPIPSITWRSTNNISSEQDLDGHWVRRHARRS--LTLSIQIRDAEGYM 385

QY 201 CSASNDVAPVRRVRYKVTNPPYISBAKGTGVVQCKTGLQCEASAVPAEFQWYKDK 260
Db 386 CTASNTIGD-QSISIDLEFQAPKLOGPAVVYTWEGNQVATICEVPAFSATISWPDGQ 444

QY 261 RLIEGK-KGVKVENRPFSLKLFENVSEHDYGNVTCVANSKLGHTNASIMLF 310
Db 445 LPPSNYSNIKIYNTSPASTLEVTPDSEDPGNVNCITAVNRIGQESLETL 495

RESULT 10
IUMSNTL
neural cell adhesion molecule 1 precursor, long domain splice form - mouse
N/Alternate names: NCAM-180
C/Species: *Mus musculus* (house mouse)
C/Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C/Accession: A29673; S00844; S00384; A28281; A44290; S00383
R/Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fontec
EMBO J. 6, 907-914, 1987
A/Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000
A/Reference number: A29673; MUID:87246524; PMID:33595563
A/Accession: A29673
A/Molecule type: mRNA
A/Residues: 1-548, 'T', 550-571, 'T', 573-574, 'D', 576-588, 'MQPS', 593, 'S', 595-599, 'P', 601, 'L',
A/Cross-references: UNIPROT:P13595; EMBL:Y00051; NID:G53342; PIDN:CAA68263.1; PID:G53343
R/Santoni, M.J.; Barthels, D.; Barbas, J.A.; Hirsch, M.R.; Steinmetz, M.; Goridis, C.; W
Nucleic Acids Res. 15, 8621-8641, 1987
A/Title: Analysis of cDNA clones that code for the transmembrane forms of the mouse neur
A/Reference number: S00844; MUID:88067687; PMID:3364567
A/Accession: S00844
A/Molecule type: mRNA
A/Residues: 529-809, 1077-1115 <SAN>
A/Cross-references: EMBL:X06328; NID:G53322; PIDN:CAA29641.1; PID:9817984
R/Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-632, 1988
A/Title: Differential splicing and alternative polyadenylation generates distinct NCAM tr

A:Reference number: S00382; MUID:88283628; PMID:3396534
 A:Accession: S00384
 A:Molecule type: DNA
 A:Residues: 642-1115 <BAR>
 A:Cross-references: EMBL:X07195
 R:Barthele, D.; Vopper, G.; Wille, W.
 Nucleic Acids Res. 16, 4217-4225, 1988
 A:Title: NCAM-180, the large isoform of the neural cell adhesion molecule of the mouse,
 A:Reference number: A28281; MUID:88247737; PMID:2454455
 A:Accession: A28281
 A:Molecule type: mRNA
 A:Residues: 804-1081 <BA3>
 A:Cross-references: EMBL:X07244; NID:953321; PIDN:CAA30230.1; PID:9929720
 R:Rougon, G.; Marahak, D.R.
 J. Biol. Chem. 261, 3396-3401, 1986
 A:Title: Structural and immunological characterization of the amino-terminal domain of n
 A:Reference number: A44290; MUID:86140120; PMID:3512556
 A:Accession: A44290
 A:Molecule type: protein
 A:Residues: 20-36 <RCU>
 C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
 C:Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:LM6
 C:Genetics:
 A:Gene: NCAM
 A:Map position: 9
 A:Intons: 643/3; 701/1; 770/2; 809/2; 1076/2
 C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
 C:Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; s1
 F:1-19/Domin: signal sequence #status predicted <SIG>
 F:20-115/Product: neural cell adhesion molecule, long domain splice form #status experi
 F:20-809,1077-1115/Product: neural cell adhesion molecule, short domain splice form #sta
 F:20-711/Domin: extracellular #status predicted <EXT>
 F:34-98/Domin: immunoglobulin homology <IMM>
 F:112-191/Domin: immunoglobulin homology <IMM2>
 F:152-156/Region: heparin binding #status predicted
 F:161-165/Region: heparin binding #status predicted
 F:228-290/Domin: immunoglobulin homology <IMM3>
 F:262-272/Region: NCAM binding #status predicted
 F:333-388/Domin: immunoglobulin homology <IMM4>
 F:420-482/Domin: immunoglobulin homology <IMM5>
 F:519-596/Domin: fibronectin type III repeat homology <FN3A>
 F:625-685/Domin: fibronectin type III repeat homology <FN3B>
 F:712-729/Domin: transmembrane #status predicted <TM>
 F:730-1115/Domin: intracellular #status predicted <INT>
 F:41-96,139-189,235-288,330-386,427-480/Denulfide bonds: #status predicted
 F:222,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.7%; Score 283.5; DB 1; Length 1115;
 Best Local Similarity 25.8%; Pred. No. 7,7e-13;
 Matches 75; Conservative 45; Mismatches 130; Indels 41; Gaps 7;

Qy 44 NVTYQGESATLRCTIDN-RVTRVAMLNRSITLYAGNDKCLDPVV-----LISNTQ 95
 Db 222 NATAKMAESVTLSCDDGFPDPPEISMLKKGPEIDGEEK-----ISFNEQSEMTI 269
 Qy 96 TVQVIEIONVNVYEGPTGCVQTDNHPKTSRVHLIYQVSPKYEISDSISINGNISL 155
 Db 269 DSEVTTANVDKNDDEAYVCAENKAGQDASHLKKFAKKITYVENQTMELBEVYTL 328
 Qy 156 TCIAATGPEPTVTR-----HISPAVGFVSEDEYLEIOGITRBOGDYE 200
 Db 329 TCBASGDPISITWRTSTRNISSEQDLGHMVVRSHARVSS---LTLKSIQYDAGSYM 385
 Qy 201 CSAANDVAAPVVRKVTVPPIYSKAKGIVGVGQKTLQCSASAVPSAEFQWYDDK 260
 Db 386 CTANSTIGQD-SQSIDLEFOYAPKLGAVAVYTWEGQVNTTCVFAPVPSXTITWFRDQ 444
 Qy 261 RLISGK-KGVVNERPFLSKLIFPNVSEHDYGNTCVASNLGHTNASIML 310
 Db 445 LIPSSNYSNIKITYTPPSASYLEVTPDSENDGNTNCTAIVRIQGESLEFIL 495

JE0099
 neural cell adhesion molecule 1 - African clawed frog
 N:Alternate names: NCAM 1
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 19-May-1998 #sequence, revision 29-May-1998 #text_change 09-Jul-2004
 C:Accession: JE0099
 R:Kido, M.; Takayama, E.; Tadakuma, T.; Shikawa, K.
 Biochem. Biophys. Res. Commun. 245, 127-132, 1998
 A:Title: Molecular cloning of sad-form neural cell adhesion molecules (N-CAMs) as the ma
 A:Reference number: JE0099; MUID:98204770; PMID:9555755
 A:Accession: JE0099
 A:Molecule type: mRNA
 A:Residues: 1-725 <KUD>
 A:Cross-references: UNIPROT:O73633; DDBJ:AB008162; NID:g3116226; PIDN:BA25931.1; PID:g311
 A:Experimental source: heart
 C:Comment: This protein mediates and regulates various cell-cell interactions through boi
 C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
 F:413-475/Domin: immunoglobulin homology <IMM>
 F:512-589/Domin: fibronectin type III repeat homology <3FR>

Query Match 15.5%; Score 279.5; DB 2; Length 725;
 Best Local Similarity 27.9%; Pred. No. 8,7e-13;
 Matches 80; Conservative 50; Mismatches 120; Indels 37; Gaps 11;

Qy 44 NVTYQGESATLRCTIDN-RVTRVAMLNRSITLYAGNDKCLDPVVLLSNTQYSIRI 102
 Db 219 NATAKMAESVTLSCDDGFPDPPEISMLKKGPEIDGEEK-----ISFNEQSEMTI 269
 Qy 103 QNVVDYDEGPTGCVQTDNHPKTSRVHLIYQVSPKYEISDSISINGNISLTCIATGR 162
 Db 270 HHEKDEAEVSCANNQAGEABEATILLKYAKRKITYVENKTAIV-ELDITTLTCEASGD 328
 Qy 163 PEPTVTV-----RHISPAV---GFVSEDEYLEIOGITRE-----QSGDYCSASNDVAAP 210
 Db 329 PISITRTAVRNISSEATTLIDGHIYKEIKHMSALTLKQIYTDABEYCIASNPICVD 388
 Qy 211 VVRKVTVNVYPYISAKGTGVPV-----GQKGLQCSASAVPSAEFQWYKDKLIE 264
 Db 389 -MQMYFEVGYAPKIR---RG---PVVVYTWEGNVNITCEVFAHPRAVVTWFRDQLPS 441
 Qy 265 GK-KGVVNERPFLSKLIFPNVSEHDYGNTCVASNLGHTNASIML 310
 Db 442 SNFSNIKIYSGPTSSSELVNPDSENDGNTNCTAINTIGHFSEFIL 488

RESULT 12
 IUCNL
 neural cell adhesion molecule long domain form precursor - chicken
 N:Alternate names: NCAM-180
 C:Contains: neural cell adhesion molecule, short domain form (NCAM-140)
 C:Species: Gallus gallus (chicken)
 C>Date: 31-Mar-1993 #sequence, revision 31-Mar-1993 #text_change 09-Jul-2004
 C:Accession: A43613; B43613; A25435; B25435; A46550; S36950; A44369; A60852; S29668
 R:Cunningham, B.A.; Hemperly, J.C.; Murray, B.A.; Prediger, B.A.; Brackenbury, R.; Edelm
 Science 236, 799-806, 1987
 A:Title: Neural cell adhesion molecule: structure, immunoglobulin-like domains, cell sur
 A:Reference number: A43613; MUID:87206190; PMID:3576139
 A:Accession: A43613
 A:Molecule type: mRNA
 A:Residues: 1-175 <CU2>
 A:Cross-references: UNIPROT:P13590; GB:M15860
 A:Accession: B43613
 A:Molecule type: protein
 A:Residues: 20-44,120-127,202-221,320-342,399-415,640-659,822-828 <CUN>
 A>Note: Asn-222 probably binds carbohydrate; Asn-226 probably does not
 R:Hemperly, J.C.; Murray, B.A.; Edelman, G.M.; Cunningham, B.A.
 Proc. Natl. Acad. Sci. U.S.A. 83, 3037-3041, 1986
 A:Title: Sequence of a cDNA clone encoding the polysialic acid-rich and cytoplasmic doma
 A:Reference number: A25435; MUID:86206089; PMID:3458261
 A:Accession: A25435
 A:Molecule type: mRNA
 A:Residues: 128-1091 <HEM>
 A:Cross-references: GB:M13210

A:Accession: B25435
A:Molecule type: protein
A:Residues: 128-140/222-240; 428-439; 611-631; 744-760; 763-781; 1080-1084 <HE2>
R:Murray, B.A.; Owens, G.C.; Prediger, E.A.; Crossin, K.L.; Cunningham, B.A.; Edelman, G.
J. Cell Biol. 103, 1431-1439, 1986
A:Title: Cell surface modulation of the neural cell adhesion molecule resulting from alternative splicing
A:Reference number: A46550; MUID:87033934; PMID:3771645
A:Accession: A46550
A:Molecule type: DNA
A:Residues: 810-1070 <MUR>
A:Cross-references: GB:X04479
R:Saenger, M.; Covault, J.
submitted to the EMBL Data Library, February 1993
A:Reference number: S36950
A:Accession: S36950
A:Molecule type: DNA
A:Residues: 1-17 <SAS>
A:Cross-references: EMBL:X70342; MUID:9417631; PIDN:CAA49807.1; PID:9417632
R:Colwell, G.; Li, B.; Forrest, D.; Brackenbury, R.
Genomics 14, 875-882, 1992
A:Title: Conserved regulatory elements in the promoter region of the N-CAM gene.
A:Reference number: A44369; MUID:93122797; PMID:1478668
A:Accession: A44369
A:Molecule type: DNA
A:Residues: 1-17 <COR>
A:Cross-references: EMBL:Z12128; MUID:963653; PIDN:CAA78113.1; PID:963654
R:Coyle, G.U.; Loewy, A.; Cross, N.V.; Akesson, R.; Glaeser, L.
J. Cell Biol. 103, 1739-1744, 1986
A:Title: Topographic localization of the heparin-binding domain of the neural cell adhesion molecule
A:Reference number: A60852; MUID:87057627; PMID:2430978
A:Accession: A60852
A:Molecule type: protein
A:Residues: 20-29 <COL>
J. Rao, Y.; Wu, X.F.; Gartezy, J.; Rutishauser, U.; Siu, C.H.
J. Cell Biol. 118, 937-949, 1992
A:Title: Identification of a peptide sequence involved in homophilic binding in the neural cell adhesion molecule
A:Reference number: A43280; MUID:92363934; PMID:11380002
A:Contents: annotation; homophilic binding region
C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM molecule
C:Comment: Various forms of NCAM are produced by alternative splicing.
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin domain
C:Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; signal sequence
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1091/Product: neural cell adhesion molecule, long domain form #status experimental
F:20-809,1071-1091/Product: neural cell adhesion molecule, short domain form #status experimental
F:120-809,1071-1091/Product: neural cell adhesion molecule, short domain form #status experimental
F:132-191/Domain: immunoglobulin homology <IMW1>
F:132-191/Domain: immunoglobulin homology <IMW2>
F:152-156/Region: heparin binding #status predicted
F:161-165/Region: heparin binding #status predicted
F:162-289/Domain: immunoglobulin homology <IMW3>
F:162-289/Domain: immunoglobulin homology <IMW4>
F:162-271/Region: NCAM binding #status experimental
F:322-387/Domain: immunoglobulin homology <IMW5>
F:419-481/Domain: immunoglobulin homology <IMW6>
F:518-595/Domain: fibronectin type III repeat homology <FN3A>
F:624-685/Domain: fibronectin type III repeat homology <FN3B>
F:712-729/Domain: transmembrane #status predicted <TM>
F:730-1091/Domain: intracellular #status predicted <INT>
F:41-96,139-189,235-287,329-385,426-479/disulfide bonds: #status predicted
F:1222/Binding site: carbohydrate (asn) (covalent) #status experimental
F:315,347,423,449,478/Binding site: carbohydrate (asn) (covalent) #status predicted

Db 256 QEDNEKSPVNDGSELIIKKDKSDSEAEYICIAENKAGQBDATIHKKVPAKPIYVEN 315

Qy 144 DISINEGNNISLTCTATGRPEPTVW----RHISPAV--GVSDEYELEIOGIREQ- 195

Db 316 KTALELEOITLTCAASGDPISITWKTSTRINSNEKILDGAIIVASHARVSSLTKEI 375

Qy 196 ---SGDYCSASNDVAAPVVRVRYVTVNPPYISEAKGTGVPVGKGTLOCEASAVPSA 251

Db 376 QYTDAGEVYCTASNTIGQD-SQAMYLEVQYAPFLQCPVAVVAYTEGNNVNITCEFAVPSA 434

Qy 252 EFQWKDKDKLLEEG-KGVKVENRPELSKLIFFNVSEHDYGNVTCVASNKLGHNTASIML 310

Db 435 VISWFRDQLLPSSNYSNIKITNTPASYLEVTPDSENDPGNYNCTAVNRIGQESSEFIL 494

RESULT 13

connectin/titin - chicken (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #ext_change 09-Jul-2004

C:Accession: T42633

R:Yajima, H.; Ohnaka, H.; Kawamura, Y.; Kume, H.; Murayama, T.; Abe, H.; Kimura, S.; May Biochem. Biophys. Res. Commun. 223, 160-164, 1996

A:Title: A 11.5-kb 5'-terminal cDNA sequence of chicken breast muscle connectin/titin re

A:Reference number: 222221; MUID:96254045; PMID:8660363

A:Accession: T42633

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-4162 <YAJ>

A:Cross-references: UNIPROT:Q98918; EMBL:D83390; NID:G1513029; PID:BAAL1908.1; PID:G151

A:Experimental source: breast muscle

C:Keywords: Skeletal muscle

Query Match 15.4%; Score 278.5; DB 2; Length 4162;

Best Local Similarity 27.3%; Pred. No. 9, 5e-12;

Matches 78; Conservative 38; Mismatches 145; Indels 25; Gaps 7;

Qy 37 TPPKAMDVTVRQGSATLACTI-DNKVTRVAMLRNSTIILYAQNDKCKLDPVVLLSQTQ 95

Db 3747 SPVKKPEEPNVLSGNTIFTSTIVKSPLEVKMFRGSIELAPGHK-----CITT 3795

Qy 96 TQYSI---EIQNVADYDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVEISDSINEGNN 152

Db 3796 LQDSVAEIELEPDVQGLQSGDYTCQVSNKAGKISCTHLLFKGEPAKFVMKVNNDLSVEKGN 3855

Qy 153 ISLTCTATGRPEPTVW----RHISPAVGSVEDEYLEIOGITREGSGDYECASN 205

Db 3856 LIIECTYGTPTPISTVTKMNGVILKHSKCSITTTETSALEIPNSKLEBOGQYCSCHEN 3915

Qy 206 DVAAVAVRVRVRYVTVNPPY-ISEAKGTGVPVGKGTLOCEASAVPSAPFQWYKODKRLIE 264

Db 3916 DSGQDNCHGA-ITLIEPPTFTVPLPEPVQVTVGDSASLQCCVAVGTPKPIVSNYKGDYTL-R 3973

Qy 265 GKKGVKVENRPELSKLIFFNVSEHDYGNVTCVASNKLGHNTASIML 310

Db 3974 GTATYKGMFKNQVATLVFSQVDSDBGYICVKENTVGEATSSLL 4019

RESULT 14

neuronal cell adhesion molecule short domain form precursor - rat

I:URNC

N:Alternate names: NCAM-140

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #ext_change 09-Jul-2004

C:Accession: S00846; B37795; I58136

R:Small, S.-J.; Shull, G.B.; Santoni, M.-J.; Akeon, R.

J:Cell Biol. 105, 2335-2345, 1987

A:Title: Identification of a cDNA clone that contains the complete coding sequence for a

A:Reference number: S00846; MUID:88059265; PMID:3680385

A:Accession: S00846

A:Molecule type: mRNA

A:Residues: 1-858 <SMA>

A:Cross-references: UNIPROT:P13596; EMBL:X06564

R.Small, S.J.; Akesson, R.
 J. Cell Biol. 111, 2089-2096, 1990
 A>Title: Expression of the unique NCAM VASE exon is independently regulated in distinct
 A/Reference number: A37795; MUID:91035620; PMID:1699951
 A/Accession: B37795
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 340-381 <SM2>
 R.Small, S.J.; Haefliger, S.L.; Akesson, R.A.
 Neuron 1, 1007-1017, 1988
 A>Title: Polypeptide variation in an N-CAM extracellular immunoglobulin-like fold is dev
 A/Reference number: 158136; MUID:90166485; PMID:2483093
 A/Accession: 158136
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 355-364 <RES>
 A/Cross-references: GB:M32611; NID:g205643; PIDN:AAA41679.1; PID:g205644
 C/Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
 C/Comment: Various forms of NCAM are produced by alternative splicing.
 C/Genetics:
 A/Gene: NCAM
 C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
 C/Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; st
 F/1-19/Domain: signal sequence #status predicted <SIG>
 F/20-858/Product: neural cell adhesion molecule, short domain form #status predicted <M
 F/20-721/Domain: extracellular #status predicted <EXT>
 F/34-98/Domain: immunoglobulin homology <IMM1>
 F/112-191/Domain: immunoglobulin homology <IMM2>
 F/152-156/Region: heparin binding #status predicted
 F/161-165/Region: heparin binding #status predicted
 F/228-290/Domain: immunoglobulin homology <IMM3>
 F/263-272/Region: NCAM binding #status predicted
 F/333-398/Domain: immunoglobulin homology <IMM4>
 F/430-492/Domain: immunoglobulin homology <IMM5>
 F/529-606/Domain: fibronectin type III repeat homology <FN3A>
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 F/722-739/Domain: transmembrane #status predicted <TM>
 F/740-658/Domain: intracellular #status predicted <INT>
 F/41-96,139-169,235-268,330-396,437-490/Denulfide bonds: #status predicted
 F/222,316,348,434,460,489/Binding site: carbohydrate (Asn) (covalent) #status predicted

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 Best Local Similarity 25.5%; Pred. No. 1.5e-12;
 Matches 75; Conservative 50; Mismatches 132; Indels 37; Gaps 7;
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 DB 222 NATNMLQOSVTLVCDAGFPPEPTSMWKDGEPIENEE---DDEKILFSDSSE--LTI 275
 QY 103 QNVVDVEGPTGCVQTDNHPKTSRVHLIVQVSPKIVEISDISINEGNNISLTCIATGR 162
 DB 276 RNVDKDEAEVYCAENKAGQDSIHLLKPAKRIITYENQTMELBEQVTLTCEASGD 335
 QY 163 PEPTVTR-----HISPAVGVSEDEYLEIQTIRBQSG 197
 DB 336 PIPSEITRTSTRNISSEKASWTRPEKQETLDGHVVRSHARVS---LTLSKIQTYPDAG 392
 QY 198 DYEGSASNDVAAPVRRVKTAVTPPYISAKGTVPGQKGTQCEASAVPSAEFQMYK 257
 DB 393 EYITTAANTIGQD-SQSNVYLEVOYAPKIQGPVAVYTEGNCQVNTTCEVFAVPSATISMFR 451
 QY 258 DDKLLIGSK-KGVAVENRPFLSKLIFNVSEHDYGTVCVANSNKGHTNASIML 310
 DB 452 DGQLLPSNSNINIKITVTPSASYLEVTPDSENDGNCTAVNRIGQESLEFIL 505

RESULT 15

JUXMLT

neural cell adhesion molecule long domain form precursor - African clawed frog
 N/Alternate names: NCAM-180
 N/Contents: neural cell adhesion molecule, short domain form (NCAM-140)
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004

C/Accession: S09600
 R/Krieg, P.A.; Sakaguchi, D.S.; Kintner, C.R.
 Nucleic Acids Res. 17, 10321-10335, 1989
 A>Title: Primary structure and developmental expression of a large cytoplasmic domain for
 A/Reference number: S09600; MUID:90098871; PMID:2481265
 A/Accession: S09600
 A/Molecule type: mRNA
 A/Residues: 1-1088 <RI>
 A/Cross-references: UNIPROT:P16170; EMBL:M25696; NID:g214609; PIDN:AAA49909.1; PID:g21461
 A/Note: the authors translated the codon AAA for residue 970 as Leu
 C/Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mole
 C/Comment: Several forms of NCAM are produced by alternative splicing.
 C/Genetics:
 A/Gene: NCAM
 C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
 C/Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; st
 F/1-19/Domain: signal sequence #status predicted <SIG>
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 F/149-153/Region: heparin binding #status predicted
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 F/225-284/Domain: immunoglobulin homology <IMM3>
 F/317-381/Domain: immunoglobulin homology <IMM4>
 F/413-475/Domain: immunoglobulin homology <IMM5>
 F/512-589/Domain: fibronectin type III repeat homology <FN3A>
 F/618-679/Domain: fibronectin type III repeat homology <FN3B>
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 F/724-1088/Domain: intracellular #status predicted <INT>
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 F/219,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.4%; Score 277.5; DB 1; Length 1088;
 Best Local Similarity 27.9%; Pred. No. 2.1e-12;
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 QY 44 NNTVROGESATLCTIDN-RTRVAMLNRSITLYAGNDKMLCDPRVLLSTQOYSIEI 102
 DB 219 NATNMAESVVLSCDADGFPDPPEISWLKGEPIEDGEK-----ISFNEQSEKTI 269
 QY 103 QNVVDVEGPTGCVQTDNHPKTSRVHLIVQVSPKIVEISDISINEGNNISLTCIATGR 162
 DB 270 HNVKDEAEVYSCANNQAGEAEATILLKYAKRIITYENKRAV-ELDEITLTCEASGD 326
 QY 163 PEPTVTR-----HISPAV---GFVSEDEYLEIQTIRE-----QSGDYBCSASNDVAAP 210
 DB 329 PIPSEITRTAVRNISSEATTLTDGHIIVKKEHIRMSALTKDIQYTDAGEYFPCIASNPICVD 388
 QY 211 VVRVKTAVTPPYISAKGTVPV-----GQKGTQCEASAVPSAEFQMYKDDKLLIE 264
 DB 389 -MQAMFEVOYAPKCI--RG--PVVVYTWEGNPNVTTCVFAHPRAAVTFRQQLPS 441
 QY 265 GK-KGVAVENRPFLSKLIFNVSEHDYGTVCVANSNKGHTNASIML 310
 DB 442 SNPSNITIKYSGPTSSSLEAVNPDSENDGNCTAVNRIGHFSEFIL 488

Search completed: June 3, 2005, 14:38:54
 Job time : 51 secs

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OM protein - protein search, using sw model

Run on: June 3, 2005, 14:20:06 / Search time 23 Seconds
(without alignments)
1116.490 Million cell updates/sec

Perfect score: 1806
Sequence: 1 MKTIQPKMNSISWAFITGL.....RRACGWLPLVLILKLF 344

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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Listing first 1500 summaries

Database : Issued Patents AA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1642	90.9	313	US-09-700-397-4	Sequence 4, Appli
3	931.5	51.6	338	US-09-976-594-404	Sequence 404, Appl
4	926.5	51.3	338	US-08-414-657D-42	Sequence 42, Appl
5	926.5	51.3	338	US-08-414-657D-43	Sequence 43, Appl
6	926.5	51.3	338	US-09-135-080-4	Sequence 4, Appli
7	923.5	51.1	325	US-08-414-657D-2	Sequence 2, Appli
8	923.5	51.1	325	US-08-414-657D-41	Sequence 41, Appl
9	923.5	51.1	325	US-09-135-080-2	Sequence 2, Appli
10	923.5	51.1	338	US-08-414-657D-60	Sequence 60, Appli
11	923.5	51.1	338	US-09-135-080-8	Sequence 8, Appli
12	908	50.3	308	US-08-414-657D-46	Sequence 46, Appli
13	907	50.2	315	US-08-414-657D-47	Sequence 47, Appli
14	905	50.1	310	US-08-414-657D-45	Sequence 45, Appli
15	902	49.9	304	US-08-414-657D-44	Sequence 44, Appli
16	886.5	49.1	287	US-08-414-657D-48	Sequence 48, Appli
17	886.5	49.0	287	US-08-414-657D-49	Sequence 49, Appli
18	796.5	44.1	252	US-08-414-657D-56	Sequence 56, Appli
19	795.5	44.0	252	US-08-414-657D-57	Sequence 57, Appli
20	742.5	41.1	212	US-09-949-016-10458	Sequence 10458, A
21	276	15.3	588	US-09-949-016-10547	Sequence 10547, A
22	267	14.8	58	US-09-513-999C-6852	Sequence 6852, Ap
23	261	14.5	1395	US-09-540-245A-15	Sequence 15, Appli
24	256	14.2	421	US-08-659-984A-1	Sequence 1, Appli
25	256	14.2	421	US-08-660-531-1	Sequence 1, Appli
26	256	14.2	444	US-08-659-984A-5	Sequence 5, Appli
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28	249.5	13.8	607	US-08-752-307B-12	Sequence 12, Appli

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30	249.5	13.8	607	US-09-991-326-12	Sequence 12, Appli
31	246.5	13.6	1018	US-08-408-093-6	Sequence 6, Appli
32	246.5	13.6	1018	US-08-408-420A-6	Sequence 6, Appli
33	246.5	13.6	1018	US-08-714-901-6	Sequence 6, Appli
34	246.5	13.6	1018	US-08-040-741-6	Sequence 6, Appli
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39	243.5	13.5	1018	US-08-452-052-2	Sequence 2, Appli
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42	237	13.1	73	US-08-414-657D-50	Sequence 50, Appli
43	237	13.1	73	US-08-414-657D-51	Sequence 51, Appli
44	230.5	12.8	868	US-08-374-834-1	Sequence 1, Appli
45	230.5	12.8	868	US-08-644-271-1	Sequence 1, Appli
46	230.5	12.8	868	US-09-077-955-1	Sequence 1, Appli
47	229.5	12.7	869	US-08-374-834-16	Sequence 16, Appli
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52	225.5	12.5	868	PCT-US95-08493-21	Sequence 21, Appli
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76	220.5	12.2	440	US-09-944-457-61	Sequence 61, Appli
77	220.5	12.2	442	US-09-778-510-20	Sequence 20, Appli
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91	213	11.8	59	US-08-414-657D-52	Sequence 52, Appli
92	212	11.7	59	US-08-414-657D-53	Sequence 53, Appli
93	211.5	11.7	1070	US-09-961-403-3	Sequence 3, Appli
94	211.5	11.7	1461	US-09-976-594-531	Sequence 531, App
95	211	11.7	398	US-09-778-510-4	Sequence 4, Appli
96	211	11.7	615	US-08-752-307B-9	Sequence 9, Appli
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99	210	11.6	191	US-09-270-767-32640	Sequence 32640, A
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106	205.5	11.4	596	US-09-991-326-13	Sequence 13, Appli
107	205	11.4	432	US-09-778-510-2	Sequence 2, Appli
108	201	11.1	946	PCT-US95-08493-13	Sequence 13, Appli
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124	192.5	10.7	907	US-09-877-730-20	Sequence 20, Appli
125	192.5	10.7	985	US-09-412-554A-2	Sequence 2, Appli
126	192.5	10.7	985	US-09-877-730-10	Sequence 10, Appli
127	192.5	10.7	991	US-09-877-730-12	Sequence 12, Appli
128	192.5	10.7	1069	US-09-877-730-2	Sequence 2, Appli
129	192.5	10.7	1072	US-09-877-730-18	Sequence 18, Appli

130	192.5	10.7	1150	4	US-09-877-730-8	Sequence 8, Appl1	203	165.5	9.2	563	2	US-08-432-016-2	Sequence 2, Appl1
131	192.5	10.7	1260	3	US-08-506-296B-21	Sequence 21, Appl1	204	165.5	9.21	563	2	US-08-684-594-2	Sequence 2, Appl1
132	192.5	10.7	1268	3	US-08-506-296B-28	Sequence 22, Appl1	205	165.5	9.2	646	4	US-09-949-016-6728	Sequence 6728, Ap
133	192	10.6	529	3	US-09-383-586-11	Sequence 31, Appl1	206	165.5	9.2	646	4	US-09-553-961-1	Sequence 4, Appl1
134	192	10.6	529	3	US-09-823-038A-31	Sequence 31, Appl1	207	165.5	9.2	828	4	US-08-261-304-2	Sequence 2, Appl1
135	191.5	10.6	1209	4	US-09-130-158A-2	Sequence 2, Appl1	208	165.5	9.2	1637	4	US-09-784-358-16	Sequence 16, Appl1
136	188.5	10.4	651	4	US-09-270-767-44877	Sequence 44877, A	209	165.5	9.2	1631	4	US-09-784-358-2	Sequence 2, Appl1
137	187.5	10.4	1266	3	US-08-506-296B-4	Sequence 4, Appl1	210	165	9.1	501	2	US-08-408-095-31	Sequence 31, Appl1
138	185.5	10.3	318	2	US-08-633-148-1	Sequence 4, Appl1	211	164	9.1	439	3	US-09-383-586-32	Sequence 32, Appl1
139	185.5	10.3	332	2	US-09-062-365-1	Sequence 1, Appl1	212	164	9.1	439	4	US-09-823-038A-32	Sequence 32, Appl1
140	185.5	10.3	340	2	US-08-633-148-2	Sequence 2, Appl1	213	164	9.1	640	4	US-09-949-016-7565	Sequence 7565, Ap
141	185.5	10.3	404	4	US-09-949-016-11025	Sequence 11025, A	214	163.5	9.1	582	4	US-09-736-457-334	Sequence 334, App
142	185.5	10.3	642	1	US-08-217-299-1	Sequence 1, Appl1	215	163.5	9.1	582	4	US-09-614-1247-334	Sequence 334, App
143	185.5	10.3	698	2	US-08-602-725-36	Sequence 36, Appl1	216	163.5	9.1	582	4	US-09-671-325-334	Sequence 334, App
144	185.5	10.3	702	4	US-09-949-016-6484	Sequence 6484, Ap	217	163.5	9.1	582	4	US-09-589-1824-334	Sequence 334, App
145	185.5	10.3	734	2	US-08-389-459A-17	Sequence 17, Appl1	218	163.5	9.1	582	4	US-09-658-884-334	Sequence 334, App
146	185.5	10.3	734	3	US-08-987-867A-17	Sequence 17, Appl1	219	163.5	9.1	582	4	US-09-658-884-334	Sequence 334, App
147	185.5	10.3	740	4	US-09-949-016-8168	Sequence 8168, Ap	220	163.5	9.1	603	4	US-09-949-016-9548	Sequence 9548, Ap
148	185	10.2	1381	3	US-09-540-245A-16	Sequence 16, Appl1	221	163.5	9.1	603	4	US-09-949-016-11206	Sequence 11206, A
149	184.5	10.2	66	2	US-08-414-657D-54	Sequence 54, Appl1	222	163.5	9.1	646	4	US-09-653-961-2	Sequence 2, Appl1
150	184.5	10.2	66	2	US-08-414-657D-55	Sequence 55, Appl1	223	163.5	9.1	1745	4	US-09-800-729-89	Sequence 89, Appl1
151	184.5	10.2	404	4	US-09-638-649-3	Sequence 3, Appl1	224	163	9.0	924	1	US-08-481-130-28	Sequence 28, Appl1
152	184.5	10.2	404	4	US-09-638-648-3	Sequence 3, Appl1	225	163	9.0	924	1	US-08-656-984A-28	Sequence 28, Appl1
153	184	10.2	373	4	US-08-823-038A-60	Sequence 60, Appl1	226	163	9.0	924	1	US-08-485-604-28	Sequence 28, Appl1
154	184	10.2	405	4	US-08-755-235-4	Sequence 4, Appl1	227	163	9.0	924	2	US-08-487-595-28	Sequence 28, Appl1
155	182	10.1	626	4	US-09-949-016-6213	Sequence 6213, Ap	228	162	9.0	331	6	5169835-17	Patent No. 5169835
156	182	10.1	664	4	US-09-949-016-7850	Sequence 7850, Ap	229	162	9.0	331	6	5169835-17	Patent No. 5169835
157	179	9.9	300	4	US-09-254-465A-10	Sequence 10, Appl1	230	161	8.9	622	4	US-09-499-846-2	Sequence 2, Appl1
158	179	9.9	300	4	US-09-397-243D-12	Sequence 12, Appl1	240	161	8.9	806	2	US-08-443-861-5	Sequence 5, Appl1
159	179	9.9	300	4	US-09-953-499-10	Sequence 10, Appl1	241	161	8.9	806	3	US-08-193-829B-5	Sequence 5, Appl1
160	174	9.6	261	4	US-09-270-767-32898	Sequence 32898, A	242	161	8.9	816	1	US-07-640-029-1	Sequence 1, Appl1
161	174	9.6	261	4	US-09-270-767-48115	Sequence 48115, A	243	161	8.9	820	1	US-07-521-807B-3	Sequence 3, Appl1
162	171.5	9.5	780	2	US-08-232-538-14	Sequence 14, Appl1	244	161	8.9	820	3	US-08-441-944A-3	Sequence 1, Appl1
163	171.5	9.5	780	2	US-08-786-164-14	Sequence 14, Appl1	245	161	8.9	820	3	US-08-439-992A-1	Sequence 2, Appl1
164	171.5	9.5	1338	4	US-08-750-141A-3	Sequence 3, Appl1	246	161	8.9	1367	2	US-08-443-861-2	Sequence 2, Appl1
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166	171	9.5	464	2	US-08-602-725-32	Sequence 32, Appl1	248	160.5	8.9	316	4	US-09-397-243D-13	Sequence 13, Appl1
167	171	9.5	464	4	US-09-949-016-6116	Sequence 6116, Ap	249	160	8.9	270	4	US-09-254-465A-24	Sequence 24, Appl1
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170	171	9.5	917	1	US-08-481-130-2	Sequence 2, Appl1	252	160	8.9	273	4	US-09-953-499-26	Sequence 26, Appl1
171	171	9.5	917	1	US-08-656-984A-2	Sequence 2, Appl1	253	160	8.9	319	3	US-08-597-495B-22	Sequence 22, Appl1
172	171	9.5	917	1	US-08-485-604-2	Sequence 2, Appl1	254	160	8.9	319	3	US-09-068-051A-22	Sequence 22, Appl1
173	171	9.5	917	2	US-08-487-595-2	Sequence 2, Appl1	255	160	8.9	319	4	US-09-536-536-67	Sequence 67, Appl1
174	171	9.5	1253	3	US-08-506-296B-14	Sequence 14, Appl1	256	160	8.9	319	4	US-09-254-465A-6	Sequence 6, Appl1
175	170	9.4	318	3	US-09-068-051A-32	Sequence 3, Appl1	257	160	8.9	319	4	US-09-953-499-6	Sequence 6, Appl1
176	167.5	9.3	280	4	US-09-270-767-43068	Sequence 43068, A	258	160	8.9	609	4	US-09-949-016-7747	Sequence 7747, Ap
177	167.5	9.3	466	2	US-08-432-016-4	Sequence 4, Appl1	259	160	8.9	609	4	US-09-949-016-7748	Sequence 7748, Ap
178	167.5	9.3	466	2	US-08-684-594-4	Sequence 4, Appl1	260	160	8.9	609	4	US-09-949-016-7749	Sequence 7749, Ap
179	167	9.2	668	1	US-08-232-538-13	Sequence 13, Appl1	261	160	8.9	609	4	US-09-949-016-7750	Sequence 7750, Ap
180	167	9.2	668	2	US-08-786-164-13	Sequence 13, Appl1	262	160	8.9	609	4	US-09-949-016-7751	Sequence 7751, Ap
181	167	9.2	764	3	US-09-142-956B-14	Sequence 14, Appl1	263	160	8.9	609	4	US-09-949-016-7752	Sequence 7752, Ap
182	167	9.2	767	2	US-08-874-678-2	Sequence 2, Appl1	264	160	8.9	609	4	US-09-949-016-7753	Sequence 7753, Ap
183	167	9.2	767	3	US-08-643-839-2	Sequence 2, Appl1	265	160	8.9	609	4	US-09-949-016-7754	Sequence 7754, Ap
184	167	9.2	767	3	US-09-348-886-2	Sequence 2, Appl1	266	160	8.9	817	1	US-07-640-029-2	Sequence 2, Appl1
185	167	9.2	788	1	US-08-232-538-15	Sequence 15, Appl1	267	160	8.9	822	1	US-07-921-807B-4	Sequence 4, Appl1
186	167	9.2	788	1	US-08-786-164-15	Sequence 15, Appl1	268	160	8.9	822	1	US-08-459-296-2	Sequence 2, Appl1
187	167	9.2	1356	1	US-08-810-116-8	Sequence 8, Appl1	269	160	8.9	822	1	US-08-441-944A-4	Sequence 4, Appl1
188	167	9.2	1356	2	US-07-930-548A-8	Sequence 2, Appl1	270	160	8.9	822	2	US-08-451-822A-12	Sequence 12, Appl1
189	167	9.2	1356	3	US-09-098-707A-2	Sequence 2, Appl1	271	160	8.9	822	3	US-08-439-992A-2	Sequence 2, Appl1
190	167	9.2	1356	3	US-09-483-539-2	Sequence 2, Appl1	272	160	8.9	822	3	US-08-323-430-12	Sequence 12, Appl1
191	167	9.2	1356	4	US-09-949-016-6198	Sequence 6198, Ap	273	159	8.8	822	1	US-07-997-133-1	Sequence 1, Appl1
192	167	9.2	1456	4	US-09-949-016-9853	Sequence 9853, Ap	274	158.5	8.8	1474	4	US-09-677-046A-4	Sequence 4, Appl1
193	166.5	9.2	302	4	US-09-877-730-14	Sequence 14, Appl1	275	158.5	8.8	292	4	US-09-677-046A-2	Sequence 2, Appl1
194	166.5	9.2	380	4	US-09-877-730-14	Sequence 14, Appl1	276	158	8.7	276	1	US-09-800-729-175	Sequence 175, App
195	166	9.2	758	2	US-08-874-678-1	Sequence 1, Appl1	277	158	8.7	611	2	US-08-752-307B-10	Sequence 10, Appl1
196	166	9.2	758	3	US-08-643-839-1	Sequence 1, Appl1	278	158	8.7	611	3	US-09-707-802-10	Sequence 10, Appl1
197	166	9.2	758	3	US-09-051-363-14	Sequence 24, Appl1	279	158	8.7	611	3	US-09-991-326-10	Sequence 10, Appl1
198	166	9.2	758	3	US-09-348-886-1	Sequence 1, Appl1	280	158	8.7	736	5	PCT-US93-00031-15	Sequence 15, Appl1
199	165.5	9.2	278	2	US-08-432-016-5	Sequence 5, Appl1	281	157.5	8.7	1503	4	US-09-677-046A-6	Sequence 6, Appl1
200	165.5	9.2	278	2	US-08-684-594-5	Sequence 5, Appl1	282	157	8.7	260	4	US-09-254-465A-23	Sequence 23, Appl1
201	165.5	9.2	466	2	US-08-432-016-6	Sequence 6, Appl1	283	157	8.7	260	4	US-09-953-499-23	Sequence 23, Appl1
202	165.5	9.2	486	2	US-08-684-594-6	Sequence 6, Appl1	284	157	8.7	263	4	US-09-254-465A-25	Sequence 25, Appl1

285	157	8.7	263	4	US-09-953-499-25	Sequence 25, Appl	367	151.5	8.4	422	4	US-08-467-602-170	Sequence 170, App
286	157	8.7	299	3	US-09-188-930-331	Sequence 331, App	368	151.5	8.4	422	4	US-08-411-295F-66	Sequence 66, Appl
287	157	8.7	299	3	US-09-463-270-2	Sequence 2, Appl1	369	151.5	8.4	422	4	US-08-411-295F-66	Sequence 66, Appl
288	157	8.7	299	4	US-09-254-465A-1	Sequence 1, Appl1	370	151.5	8.4	422	4	US-08-411-295F-69	Sequence 69, Appl
289	157	8.7	299	4	US-09-312-283C-189	Sequence 189, App	371	151.5	8.4	422	4	US-08-411-295F-103	Sequence 103, App
290	157	8.7	299	4	US-09-312-283C-331	Sequence 331, App	372	151.5	8.4	422	5	PCT-US94-05083C-166	Sequence 166, App
294	157	8.7	299	4	US-09-397-243D-3	Sequence 3, Appl1	373	151.5	8.4	422	5	PCT-US94-05083C-185	Sequence 185, App
301	157	8.7	299	4	US-09-953-499-1	Sequence 1, Appl1	374	151.5	8.4	422	5	PCT-US95-06846A-170	Sequence 170, App
302	156.5	8.7	416	4	US-09-638-649-1	Sequence 1, Appl1	375	151.5	8.4	1363	2	US-08-874-678-32	Sequence 32, Appl
303	156.5	8.7	416	4	US-08-755-235-2	Sequence 2, Appl1	376	151.5	8.4	1363	3	US-08-643-839-32	Sequence 32, Appl
304	156.5	8.7	416	4	US-09-638-648-1	Sequence 1, Appl1	377	151.5	8.4	1363	3	US-09-348-886-32	Sequence 32, Appl
305	155.5	8.6	299	3	US-09-188-930-189	Sequence 189, App	378	151	8.4	874	2	US-08-456-647B-6	Sequence 6, Appl1
306	155.5	8.6	880	3	US-08-445-640-10	Sequence 10, Appl	379	151	8.4	874	2	US-08-237-401A-6	Sequence 4, Appl1
307	155.5	8.6	880	3	US-08-170-558-10	Sequence 10, Appl	380	150.5	8.3	349	4	US-09-924-103-4	Sequence 4, Appl1
308	155.5	8.6	880	3	US-08-447-314-10	Sequence 10, Appl	381	150.5	8.3	411	3	US-08-470-339-189	Sequence 189, App
309	155.5	8.6	880	3	US-08-445-641-10	Sequence 10, Appl	382	150.5	8.3	414	3	US-08-470-339-188	Sequence 188, App
310	155.5	8.6	880	4	US-09-223-490-10	Sequence 10, Appl	383	150.5	8.3	422	4	US-08-467-602-324	Sequence 324, App
311	155	8.6	805	3	US-08-985-526-34	Sequence 34, Appl	384	150.5	8.3	422	4	US-08-411-295F-250	Sequence 250, App
312	155	8.6	1248	4	US-09-949-016-10595	Sequence 10595, A	385	150.5	8.3	425	3	US-08-470-335-326	Sequence 326, App
313	155	8.6	1248	4	US-09-949-016-10596	Sequence 10596, A	386	150.5	8.3	425	4	US-08-467-602-320	Sequence 320, App
314	155	8.6	1363	4	US-09-375-248-19	Sequence 19, Appl	387	150.5	8.3	425	4	US-08-411-295F-246	Sequence 246, App
315	155	8.6	1367	1	US-07-813-593-4	Sequence 4, Appl1	388	150.5	8.3	445	4	US-08-467-602-328	Sequence 328, App
316	155	8.6	1367	1	US-07-977-451-6	Sequence 6, Appl1	389	150.5	8.3	445	4	US-08-411-295F-254	Sequence 254, App
317	155	8.6	1367	1	US-07-946-507-4	Sequence 4, Appl1	390	150.5	8.3	456	4	US-08-467-602-366	Sequence 366, App
318	155	8.6	1367	1	US-08-253-517-6	Sequence 6, Appl1	391	150.5	8.3	456	4	US-08-411-295F-292	Sequence 292, App
319	155	8.6	1367	1	US-07-906-397A-6	Sequence 6, Appl1	392	150.5	8.3	459	4	US-08-467-602-362	Sequence 362, App
320	155	8.6	1367	1	US-08-601-891-6	Sequence 6, Appl1	393	150.5	8.3	459	4	US-08-411-295F-288	Sequence 288, App
321	155	8.6	1367	2	US-09-021-324-6	Sequence 6, Appl1	394	150.5	8.3	479	4	US-08-467-602-370	Sequence 370, App
322	155	8.6	1367	4	US-09-872-136B-6	Sequence 6, Appl1	395	150.5	8.3	479	4	US-08-411-295F-296	Sequence 296, App
323	155	8.6	1367	5	PCT-US92-02750-8	Sequence 8, Appl1	396	150.5	8.3	601	3	US-08-470-335-233	Sequence 233, App
324	155	8.6	1367	5	PCT-US92-05401-6	Sequence 6, Appl1	397	150.5	8.3	601	4	US-08-467-602-323	Sequence 323, App
325	155	8.6	1367	5	PCT-US92-09893-6	Sequence 6, Appl1	398	150.5	8.3	601	4	US-08-411-295F-249	Sequence 249, App
326	154.5	8.6	462	2	US-08-752-307B-7	Sequence 7, Appl1	399	150.5	8.3	604	3	US-08-470-335-227	Sequence 227, App
327	154.5	8.6	462	3	US-09-707-802-7	Sequence 7, Appl1	400	150.5	8.3	604	4	US-08-467-602-318	Sequence 318, App
328	154.5	8.6	462	3	US-09-991-326-7	Sequence 7, Appl1	401	150.5	8.3	604	4	US-08-411-295F-244	Sequence 244, App
329	154.5	8.6	465	2	US-08-752-307B-5	Sequence 5, Appl1	402	150.5	8.3	610	3	US-08-470-335-236	Sequence 236, App
330	154.5	8.6	465	3	US-09-707-802-5	Sequence 5, Appl1	403	150.5	8.3	610	4	US-08-467-602-332	Sequence 332, App
331	154.5	8.6	465	3	US-09-991-326-5	Sequence 5, Appl1	404	150.5	8.3	610	4	US-08-411-295F-258	Sequence 258, App
332	154.5	8.6	602	1	US-08-428-926-5	Sequence 5, Appl1	405	150.5	8.3	613	3	US-08-470-335-230	Sequence 230, App
333	154.5	8.6	602	1	US-08-428-927-5	Sequence 5, Appl1	406	150.5	8.3	613	4	US-08-467-602-329	Sequence 329, App
334	154.5	8.6	602	1	US-08-428-298-5	Sequence 5, Appl1	407	150.5	8.3	613	4	US-08-411-295F-255	Sequence 255, App
335	154.5	8.6	602	1	US-08-339-517-5	Sequence 5, Appl1	408	150.5	8.3	624	4	US-08-467-602-326	Sequence 326, App
336	154.5	8.6	1311	3	US-08-340-011-5	Sequence 5, Appl1	409	150.5	8.3	624	4	US-08-411-295F-252	Sequence 252, App
337	154.5	8.6	1311	3	US-08-901-710-5	Sequence 5, Appl1	410	150.5	8.3	633	4	US-08-467-602-335	Sequence 335, App
338	154.5	8.6	1311	4	US-09-169-079-5	Sequence 5, Appl1	411	150.5	8.3	633	4	US-08-411-295F-261	Sequence 261, App
339	154	8.5	579	3	US-09-173-151A-2	Sequence 2, Appl1	412	150.5	8.3	635	4	US-08-467-602-365	Sequence 365, App
340	154	8.5	579	3	US-09-173-151A-4	Sequence 4, Appl1	413	150.5	8.3	635	4	US-08-411-295F-291	Sequence 291, App
341	153.5	8.5	477	2	US-08-432-016-3	Sequence 3, Appl1	414	150.5	8.3	638	4	US-08-467-602-360	Sequence 360, App
342	153.5	8.5	477	2	US-08-684-594-3	Sequence 3, Appl1	415	150.5	8.3	638	4	US-08-411-295F-286	Sequence 286, App
343	153	8.5	189	4	US-09-270-767-32726	Sequence 32726, A	416	150.5	8.3	644	4	US-08-467-602-374	Sequence 374, App
344	153	8.5	189	4	US-09-270-767-47943	Sequence 47943, A	417	150.5	8.3	644	4	US-08-411-295F-300	Sequence 300, App
345	153	8.5	524	4	US-09-270-767-44009	Sequence 44009, A	418	150.5	8.3	647	4	US-08-467-602-371	Sequence 371, App
346	153	8.5	894	4	US-09-949-016-10605	Sequence 10605, A	419	150.5	8.3	647	4	US-08-411-295F-297	Sequence 297, App
347	152	8.4	351	5	PCT-US93-05703-2	Sequence 2, Appl1	420	150.5	8.3	658	4	US-08-467-602-368	Sequence 368, App
348	152	8.4	1123	4	US-09-949-016-6230	Sequence 6230, App	421	150.5	8.3	658	4	US-08-411-295F-294	Sequence 294, App
349	152	8.4	1128	4	US-09-949-016-7522	Sequence 7522, App	422	150.5	8.3	667	4	US-08-467-602-377	Sequence 377, App
350	151.5	8.4	227	4	US-09-205-258-947	Sequence 947, App	423	150.5	8.3	777	2	US-08-411-295F-303	Sequence 303, App
351	151.5	8.4	422	1	US-09-949-016-7591	Sequence 7591, App	424	150.5	8.3	777	3	US-08-874-678-3	Sequence 3, Appl1
352	151.5	8.4	422	1	US-08-036-555B-170	Sequence 170, App	425	150.5	8.3	777	3	US-08-643-839-3	Sequence 3, Appl1
353	151.5	8.4	422	1	US-08-469-569-170	Sequence 170, App	426	150.5	8.3	777	3	US-09-348-886-3	Sequence 3, Appl1
354	151.5	8.4	422	1	US-08-428-926-3	Sequence 3, Appl1	427	150.5	8.3	818	3	US-08-470-335-233	Sequence 233, App
355	151.5	8.4	422	1	US-08-249-332A-170	Sequence 170, App	428	150.5	8.3	818	4	US-08-467-602-321	Sequence 321, App
356	151.5	8.4	422	1	US-08-428-927-3	Sequence 3, Appl1	429	150.5	8.3	818	4	US-08-411-295F-247	Sequence 247, App
357	151.5	8.4	422	1	US-08-428-298-3	Sequence 3, Appl1	430	150.5	8.3	821	3	US-08-470-335-228	Sequence 228, App
358	151.5	8.4	422	1	US-08-339-517-3	Sequence 3, Appl1	431	150.5	8.3	821	4	US-08-467-602-319	Sequence 319, App
359	151.5	8.4	422	1	US-08-469-526A-170	Sequence 170, App	432	150.5	8.3	821	4	US-08-411-295F-245	Sequence 245, App
360	151.5	8.4	422	2	US-08-734-591A-170	Sequence 170, App	433	150.5	8.3	827	3	US-08-470-335-237	Sequence 237, App
361	151.5	8.4	422	2	US-08-469-660-170	Sequence 170, App	434	150.5	8.3	827	4	US-08-467-602-333	Sequence 333, App
362	151.5	8.4	422	3	US-08-341-018-72	Sequence 72, Appl	435	150.5	8.3	827	4	US-08-411-295F-259	Sequence 259, App
363	151.5	8.4	422	3	US-08-470-335-170	Sequence 170, App	436	150.5	8.3	830	3	US-08-470-335-231	Sequence 231, App
364	151.5	8.4	422	3	US-08-735-021-170	Sequence 170, App	437	150.5	8.3	830	4	US-08-467-602-330	Sequence 330, App
365	151.5	8.4	422	3	US-08-734-664A-170	Sequence 170, App	438	150.5	8.3	830	4	US-08-411-295F-256	Sequence 256, App
366	151.5	8.4	422	3	US-08-470-339-170	Sequence 170, App	439	150.5	8.3	841	4	US-08-467-602-327	Sequence 327, App

440	150.5	8.3	841	4	US-08-411-295F-253	Sequence 253, App	513	147.5	8.2	403	4	US-09-638-648-5	Sequence 5, Appl1
441	150.5	8.3	850	4	US-08-467-602-336	Sequence 336, App	514	145.5	8.1	232	4	US-09-270-767-44627	Sequence 44627, A
442	150.5	8.3	850	4	US-08-411-295F-262	Sequence 262, App	515	145.5	8.1	549	4	US-09-858-664A-5	Sequence 5, Appl1
443	150.5	8.3	852	4	US-08-467-602-363	Sequence 363, App	516	145.5	8.1	549	4	US-10-274-978-6	Sequence 6, Appl1
444	150.5	8.3	852	4	US-08-411-295F-289	Sequence 289, App	517	145.5	8.1	549	4	US-10-697-263-6	Sequence 6, Appl1
445	150.5	8.3	855	4	US-08-467-602-361	Sequence 361, App	518	145	8.0	972	3	US-08-750-141A-2	Sequence 2, Appl1
446	150.5	8.3	855	4	US-08-411-295F-287	Sequence 287, App	519	145	8.0	972	4	US-09-944-807-10	Sequence 10, Appl1
447	150.5	8.3	861	4	US-08-467-602-375	Sequence 375, App	520	144	8.0	972	4	US-09-945-473B-25	Sequence 25, Appl1
448	150.5	8.3	861	4	US-08-411-295F-301	Sequence 301, App	521	143.5	7.9	344	2	US-08-602-725-34	Sequence 74, Appl1
449	150.5	8.3	864	4	US-08-467-602-372	Sequence 372, App	522	143.5	7.9	662	1	US-08-661-304-7	Sequence 7, Appl1
450	150.5	8.3	864	4	US-08-411-295F-298	Sequence 298, App	523	143	7.9	661	1	US-08-232-538-12	Sequence 12, Appl1
451	150.5	8.3	865	3	US-08-470-335-235	Sequence 235, App	524	143	7.9	661	2	US-08-786-164-12	Sequence 12, Appl1
452	150.5	8.3	865	4	US-08-467-602-222	Sequence 322, App	525	143	7.9	667	1	US-08-232-538-6	Sequence 6, Appl1
453	150.5	8.3	865	4	US-08-411-295F-228	Sequence 228, App	526	143	7.9	667	2	US-08-786-164-6	Sequence 6, Appl1
454	150.5	8.3	868	3	US-08-470-335-229	Sequence 229, App	527	143	7.9	667	3	US-09-427-353-2	Sequence 2, Appl1
455	150.5	8.3	868	4	US-08-467-602-317	Sequence 317, App	528	142.5	7.9	263	4	US-08-411-295F-77	Sequence 77, Appl1
456	150.5	8.3	868	4	US-08-411-295F-243	Sequence 243, App	529	142.5	7.9	411	4	US-09-592-998C-9	Sequence 9, Appl1
457	150.5	8.3	874	3	US-08-470-335-338	Sequence 238, App	530	142.5	7.9	435	4	US-09-592-998C-10	Sequence 10, Appl1
458	150.5	8.3	874	4	US-08-467-602-334	Sequence 334, App	531	142.5	7.9	735	5	PCT-US93-00031-13	Sequence 13, Appl1
459	150.5	8.3	874	4	US-08-411-295F-260	Sequence 260, App	532	142.5	7.9	739	3	US-08-482-073-6	Sequence 6, Appl1
460	150.5	8.3	875	4	US-08-467-602-369	Sequence 369, App	533	142.5	7.9	739	5	US-08-482-073-6	Sequence 9, Appl1
461	150.5	8.3	875	4	US-08-411-295F-295	Sequence 295, App	534	141.5	7.8	254	3	US-08-470-335-193	Sequence 193, App
462	150.5	8.3	877	3	US-08-470-335-232	Sequence 232, App	535	141.5	7.8	257	3	US-08-341-018-6	Sequence 6, Appl1
463	150.5	8.3	877	4	US-08-467-602-331	Sequence 331, App	536	141.5	7.8	257	3	US-08-470-339-193	Sequence 193, App
464	150.5	8.3	877	4	US-08-411-295F-257	Sequence 257, App	537	141.5	7.8	257	4	US-08-467-602-387	Sequence 387, App
465	150.5	8.3	884	4	US-08-467-602-378	Sequence 378, App	538	141.5	7.8	257	4	US-08-411-295F-6	Sequence 6, Appl1
466	150.5	8.3	884	4	US-08-411-295F-304	Sequence 304, App	539	141.5	7.8	263	4	US-08-411-295F-4	Sequence 4, Appl1
467	150.5	8.3	888	4	US-08-467-602-325	Sequence 325, App	540	141.5	7.8	280	3	US-08-341-018-56	Sequence 56, Appl1
468	150.5	8.3	888	4	US-08-411-295F-251	Sequence 251, App	541	141.5	7.8	280	3	US-08-470-335-192	Sequence 192, App
469	150.5	8.3	897	4	US-08-467-602-337	Sequence 337, App	542	141.5	7.8	280	3	US-08-470-339-192	Sequence 192, App
470	150.5	8.3	897	4	US-08-411-295F-263	Sequence 263, App	543	141.5	7.8	280	4	US-08-467-602-386	Sequence 386, App
471	150.5	8.3	899	4	US-08-467-602-364	Sequence 364, App	544	141.5	7.8	280	4	US-08-411-295F-49	Sequence 49, Appl1
472	150.5	8.3	899	4	US-08-411-295F-290	Sequence 290, App	545	141.5	7.8	280	4	US-08-411-295F-95	Sequence 95, Appl1
473	150.5	8.3	902	4	US-08-467-602-359	Sequence 359, App	546	141.5	7.8	388	1	US-08-445-640-12	Sequence 12, Appl1
474	150.5	8.3	902	4	US-08-411-295F-285	Sequence 285, App	547	141.5	7.8	388	3	US-08-170-558-12	Sequence 12, Appl1
475	150.5	8.3	908	4	US-08-467-602-376	Sequence 376, App	548	141.5	7.8	388	3	US-08-447-314-12	Sequence 12, Appl1
476	150.5	8.3	908	4	US-08-411-295F-302	Sequence 302, App	549	141.5	7.8	388	3	US-08-445-461-12	Sequence 12, Appl1
477	150.5	8.3	911	4	US-08-467-602-373	Sequence 373, App	550	141.5	7.8	388	4	US-09-223-490-12	Sequence 12, Appl1
478	150.5	8.3	911	4	US-08-411-295F-299	Sequence 299, App	551	141	7.8	471	4	US-09-949-016-9042	Sequence 9042, Ap
479	150.5	8.3	922	4	US-08-467-602-367	Sequence 367, App	552	141	7.8	471	4	US-09-949-016-9043	Sequence 9043, Ap
480	150.5	8.3	922	4	US-08-411-295F-293	Sequence 293, App	553	141	7.8	471	4	US-09-949-016-9044	Sequence 9044, Ap
481	150.5	8.3	931	4	US-08-467-602-379	Sequence 379, App	554	141	7.8	471	4	US-09-949-016-9045	Sequence 9045, Ap
482	150.5	8.3	931	4	US-08-411-295F-305	Sequence 305, App	555	141	7.8	471	4	US-09-949-016-9046	Sequence 9046, Ap
483	150.5	8.3	1298	1	US-08-222-616-53	Sequence 33, Appl	556	141	7.8	471	4	US-09-949-016-9047	Sequence 9047, Ap
484	150.5	8.3	1298	1	US-08-340-011-2	Sequence 2, Appl1	557	141	7.8	471	4	US-09-949-016-9048	Sequence 9048, Ap
485	150.5	8.3	1298	1	US-08-901-710-2	Sequence 2, Appl1	558	141	7.8	471	4	US-09-949-016-9049	Sequence 9049, Ap
486	150.5	8.3	1298	3	US-08-446-648-33	Sequence 33, Appl	559	141	7.8	471	4	US-09-949-016-9051	Sequence 9050, Ap
487	150.5	8.3	1298	4	US-09-982-610-33	Sequence 33, Appl	560	141	7.8	471	4	US-09-949-016-9051	Sequence 9051, Ap
488	150.5	8.3	1298	4	US-09-169-079-2	Sequence 2, Appl1	561	141	7.8	821	2	US-08-451-822A-13	Sequence 13, Appl
489	150.5	8.3	1298	5	PCT-US95-04228-33	Sequence 33, Appl	562	141	7.8	821	3	US-08-323-430-13	Sequence 13, Appl
490	150.5	8.3	1362	2	US-08-874-678-33	Sequence 33, Appl	563	140.5	7.8	821	3	US-08-411-295F-78	Sequence 78, Appl
491	150.5	8.3	1362	3	US-08-643-839-33	Sequence 33, Appl	564	140.5	7.8	552	4	US-09-969-532-6	Sequence 6, Appl1
492	150.5	8.3	1362	3	US-09-348-886-33	Sequence 33, Appl	565	140.5	7.8	553	4	US-09-969-532-6	Sequence 6, Appl1
493	150.5	8.3	1363	1	US-08-340-011-4	Sequence 4, Appl1	566	140.5	7.8	566	4	US-09-969-532-2	Sequence 2, Appl1
494	150.5	8.3	1363	3	US-08-901-710-4	Sequence 4, Appl1	567	140.5	7.8	571	4	US-09-969-532-2	Sequence 2, Appl1
495	150.5	8.3	1363	3	US-09-375-248-2	Sequence 2, Appl1	568	140.5	7.8	589	4	US-09-866-510-12	Sequence 12, Appl1
496	150.5	8.3	1363	4	US-09-169-079-4	Sequence 4, Appl1	569	140.5	7.8	762	4	US-09-949-016-7568	Sequence 7568, Ap
497	150.5	8.3	1368	2	US-08-874-678-34	Sequence 34, Appl	570	140.5	7.8	886	4	US-09-969-532-16	Sequence 16, Appl
498	150.5	8.3	1368	3	US-08-643-839-34	Sequence 34, Appl	571	140.5	7.8	897	4	US-09-969-532-12	Sequence 12, Appl
499	150.5	8.3	1368	3	US-09-348-886-34	Sequence 34, Appl	572	140.5	7.8	900	4	US-09-969-532-14	Sequence 14, Appl
500	150	8.3	355	1	US-08-471-570-14	Sequence 14, Appl	573	140.5	7.8	911	4	US-09-969-532-10	Sequence 10, Appl
501	150	8.3	643	1	US-08-471-570-6	Sequence 6, Appl1	574	140.5	7.8	911	4	US-09-961-403-4	Sequence 4, Appl1
502	150	8.3	769	1	US-08-471-570-8	Sequence 8, Appl1	575	140.5	7.8	1089	1	US-08-180-195-36	Sequence 36, Appl
503	149.5	8.3	1501	2	US-08-447-464-3	Sequence 3, Appl1	576	140.5	7.8	1089	1	US-08-168-917-4	Sequence 4, Appl1
504	149.5	8.3	1501	2	US-08-716-679-3	Sequence 3, Appl1	577	140.5	7.8	1089	1	US-08-477-329-36	Sequence 36, Appl
505	149	8.3	388	1	US-08-429-742-4	Sequence 4, Appl1	578	140.5	7.8	1089	2	US-08-475-458-36	Sequence 36, Appl
506	148.5	8.2	1911	1	US-08-348-006B-5	Sequence 5, Appl1	579	140.5	7.8	1089	2	US-08-460-510-4	Sequence 4, Appl1
507	148.5	8.2	1911	2	US-08-800-825A-5	Sequence 5, Appl1	580	140.5	7.8	1089	2	US-08-460-490-4	Sequence 4, Appl1
508	148.5	8.2	1911	3	US-09-158-657-5	Sequence 5, Appl1	581	140.5	7.8	1089	3	US-08-980-400-36	Sequence 36, Appl
509	148.5	8.2	1911	5	PCT-US94-10166-5	Sequence 5, Appl1	582	140.5	7.8	1089	3	US-08-462-728-2	Sequence 2, Appl1
510	148	8.2	602	1	US-08-168-091A-2	Sequence 2, Appl1	583	140.5	7.8	1089	3	US-09-583-459A-36	Sequence 36, Appl
511	148	8.2	820	1	US-08-166-717D-6	Sequence 6, Appl1	584	140.5	7.8	1089	3	US-09-583-210-36	Sequence 36, Appl
512	147.5	8.2	403	4	US-09-638-649-5	Sequence 5, Appl1	585	140.5	7.8	1089	3	US-09-583-449A-36	Sequence 36, Appl

586	140.5	7.8	1089	3	US-09-435-059-36	Sequence 36, Appl	659	138.5	7.7	572	4	US-08-411-295F-161	Sequence 161, App
587	140.5	7.8	1089	3	US-08-461-917-2	Sequence 2, Appl	660	138.5	7.7	578	4	US-08-467-602-249	Sequence 249, App
588	140.5	7.8	1089	4	US-08-464-436-2	Sequence 2, Appl	661	138.5	7.7	578	4	US-08-411-295F-175	Sequence 175, App
589	140.5	7.8	1089	4	US-08-464-436-2	Sequence 2, Appl	662	138.5	7.7	581	4	US-08-467-602-246	Sequence 246, App
590	140.5	7.8	1089	4	US-09-769-987-2	Sequence 2, Appl	663	138.5	7.7	581	4	US-08-411-295F-172	Sequence 172, App
591	140.5	7.8	1089	4	US-09-866-510-2	Sequence 2, Appl	664	138.5	7.7	592	4	US-08-467-602-243	Sequence 243, App
592	140.5	7.8	1089	4	US-09-866-510-4	Sequence 4, Appl	665	138.5	7.7	592	4	US-08-411-295F-169	Sequence 169, App
593	140.5	7.8	1089	4	US-09-866-510-6	Sequence 6, Appl	666	138.5	7.7	601	4	US-08-467-602-252	Sequence 252, App
594	140.5	7.8	1089	4	US-09-866-510-8	Sequence 8, Appl	667	138.5	7.7	601	4	US-08-411-295F-178	Sequence 178, App
595	140.5	7.8	1089	4	US-09-866-510-10	Sequence 10, Appl	668	138.5	7.7	603	4	US-08-467-602-279	Sequence 279, App
596	140.5	7.8	1089	4	US-09-919-497-90	Sequence 90, Appl	669	138.5	7.7	603	4	US-08-411-295F-205	Sequence 205, App
597	140.5	7.8	1089	4	US-09-949-016-6703	Sequence 6703, Ap	670	138.5	7.7	606	4	US-08-467-602-277	Sequence 277, App
598	140.5	7.8	1089	5	PCT-US92-00730-4	Sequence 4, Appl	671	138.5	7.7	606	4	US-08-411-295F-203	Sequence 203, App
599	140.5	7.8	1089	5	PCT-US92-00862-4	Sequence 4, Appl	672	138.5	7.7	612	4	US-08-467-602-291	Sequence 291, App
600	140	7.8	203	4	US-09-270-767-60345	Sequence 60345, A	673	138.5	7.7	612	4	US-08-411-295F-217	Sequence 217, App
601	140	7.8	801	3	US-09-383-630-6	Sequence 6, Appl	674	138.5	7.7	615	4	US-08-467-602-288	Sequence 288, App
602	140	7.8	890	1	US-08-445-640-2	Sequence 2, Appl	675	138.5	7.7	615	4	US-08-411-295F-214	Sequence 214, App
603	140	7.8	890	3	US-08-170-558-2	Sequence 2, Appl	676	138.5	7.7	616	4	US-08-467-602-238	Sequence 238, App
604	140	7.8	890	3	US-08-447-314-2	Sequence 2, Appl	677	138.5	7.7	616	4	US-08-411-295F-164	Sequence 164, App
605	140	7.8	890	3	US-08-445-461-2	Sequence 2, Appl	678	138.5	7.7	619	4	US-08-467-602-233	Sequence 233, App
606	140	7.8	890	4	US-09-223-480-2	Sequence 2, Appl	679	138.5	7.7	619	4	US-08-411-295F-159	Sequence 159, App
607	140	7.8	911	1	US-08-286-305A-1	Sequence 1, Appl	680	138.5	7.7	625	4	US-08-467-602-250	Sequence 250, App
608	140	7.8	911	2	US-08-441-104A-1	Sequence 1, Appl	681	138.5	7.7	625	4	US-08-411-295F-176	Sequence 176, App
609	140	7.8	911	2	US-08-440-816A-1	Sequence 1, Appl	682	138.5	7.7	626	4	US-08-467-602-285	Sequence 285, App
610	140	7.8	911	3	US-09-417-381A-1	Sequence 1, Appl	683	138.5	7.7	626	4	US-08-411-295F-211	Sequence 211, App
611	140	7.8	976	3	US-08-750-141A-1	Sequence 1, Appl	684	138.5	7.7	628	4	US-08-467-602-247	Sequence 247, App
612	139.5	7.7	263	3	US-08-341-018-4	Sequence 4, Appl	685	138.5	7.7	628	4	US-08-411-295F-173	Sequence 173, App
613	139.5	7.7	263	3	US-08-470-335-191	Sequence 191, App	686	138.5	7.7	635	4	US-08-467-602-294	Sequence 294, App
614	139.5	7.7	263	3	US-08-470-339-191	Sequence 191, App	687	138.5	7.7	639	4	US-08-411-295F-220	Sequence 220, App
615	139.5	7.7	263	3	US-08-467-602-385	Sequence 385, App	688	138.5	7.7	639	4	US-08-467-602-241	Sequence 241, App
616	139.5	7.7	419	6	5169835-2	Patent No. 5169835	689	138.5	7.7	648	4	US-08-467-602-253	Sequence 253, App
617	139.5	7.7	419	6	5169835-2	Patent No. 5169835	690	138.5	7.7	648	4	US-08-411-295F-179	Sequence 179, App
618	139	7.7	272	1	US-08-282-951-6	Sequence 6, Appl	691	138.5	7.7	650	4	US-08-467-602-280	Sequence 280, App
619	138.5	7.7	140	3	US-08-986-485-4	Sequence 4, Appl	692	138.5	7.7	650	4	US-08-411-295F-206	Sequence 206, App
620	138.5	7.7	173	4	US-08-467-602-240	Sequence 240, App	693	138.5	7.7	650	4	US-08-467-602-275	Sequence 275, App
621	138.5	7.7	173	4	US-08-411-295F-166	Sequence 166, App	694	138.5	7.7	653	4	US-08-467-602-201	Sequence 201, App
622	138.5	7.7	176	4	US-08-467-602-236	Sequence 236, App	695	138.5	7.7	653	4	US-08-411-295F-201	Sequence 201, App
623	138.5	7.7	176	4	US-08-411-295F-162	Sequence 162, App	696	138.5	7.7	659	4	US-08-467-602-292	Sequence 292, App
624	138.5	7.7	196	4	US-08-467-602-244	Sequence 244, App	697	138.5	7.7	659	4	US-08-411-295F-218	Sequence 218, App
625	138.5	7.7	196	4	US-08-411-295F-170	Sequence 170, App	698	138.5	7.7	662	4	US-08-467-602-289	Sequence 289, App
626	138.5	7.7	207	4	US-08-467-602-282	Sequence 282, App	699	138.5	7.7	662	4	US-08-411-295F-215	Sequence 215, App
627	138.5	7.7	207	4	US-08-411-295F-208	Sequence 208, App	700	138.5	7.7	673	4	US-08-467-602-283	Sequence 283, App
628	138.5	7.7	210	4	US-08-467-602-278	Sequence 278, App	701	138.5	7.7	673	4	US-08-411-295F-209	Sequence 209, App
629	138.5	7.7	210	4	US-08-411-295F-204	Sequence 204, App	702	138.5	7.7	682	4	US-08-467-602-295	Sequence 295, App
630	138.5	7.7	230	4	US-08-467-602-286	Sequence 286, App	703	138.5	7.7	682	4	US-08-411-295F-221	Sequence 221, App
631	138.5	7.7	230	4	US-08-411-295F-212	Sequence 212, App	704	137	7.6	514	4	US-09-949-016-11380	Sequence 11380, A
632	138.5	7.7	352	4	US-08-467-602-239	Sequence 239, App	705	137	7.6	514	4	US-09-723-368-4	Sequence 4, Appl
633	138.5	7.7	352	4	US-08-411-295F-165	Sequence 165, App	706	136.5	7.6	388	1	US-08-445-640-6	Sequence 6, Appl
634	138.5	7.7	355	4	US-08-467-602-234	Sequence 234, App	707	136.5	7.6	388	3	US-08-170-558-6	Sequence 6, Appl
635	138.5	7.7	355	4	US-08-411-295F-160	Sequence 160, App	708	136.5	7.6	388	3	US-08-447-314-6	Sequence 6, Appl
636	138.5	7.7	361	4	US-08-467-602-248	Sequence 248, App	709	136.5	7.6	388	3	US-08-445-461-6	Sequence 6, Appl
637	138.5	7.7	361	4	US-08-411-295F-174	Sequence 174, App	710	136.5	7.6	388	4	US-09-222-490-6	Sequence 4, Appl
638	138.5	7.7	364	4	US-08-467-602-245	Sequence 245, App	711	136.5	7.6	498	4	US-09-354-151-2	Sequence 2, Appl
639	138.5	7.7	364	4	US-08-411-295F-171	Sequence 171, App	712	136.5	7.6	738	3	US-08-478-208-32	Sequence 32, Appl
640	138.5	7.7	375	4	US-08-467-602-242	Sequence 242, App	713	136.5	7.6	738	3	US-09-336-536-73	Sequence 73, Appl
641	138.5	7.7	375	4	US-08-411-295F-168	Sequence 168, App	714	136.5	7.6	738	6	5264554-2	Patent No. 5264554
642	138.5	7.7	384	4	US-08-467-602-251	Sequence 251, App	715	136.5	7.6	738	6	5264554-2	Patent No. 5264554
643	138.5	7.7	384	4	US-08-411-295F-177	Sequence 177, App	716	136	7.5	393	1	US-08-429-742-2	Sequence 2, Appl
644	138.5	7.7	386	4	US-08-467-602-281	Sequence 281, App	717	136	7.5	458	4	US-09-435-956A-1	Sequence 1, Appl
645	138.5	7.7	386	4	US-08-411-295F-207	Sequence 207, App	718	136	7.5	644	5	PCT-US93-00031-21	Sequence 21, Appl
646	138.5	7.7	389	4	US-08-467-602-276	Sequence 276, App	719	135.5	7.5	371	4	US-08-411-295F-308	Sequence 308, App
647	138.5	7.7	389	4	US-08-411-295F-202	Sequence 202, App	720	135.5	7.5	405	4	US-08-467-602-284	Sequence 284, App
648	138.5	7.7	395	4	US-08-467-602-280	Sequence 280, App	721	135.5	7.5	405	4	US-08-411-295F-307	Sequence 307, App
649	138.5	7.7	395	4	US-08-411-295F-216	Sequence 216, App	722	135.5	7.5	501	3	US-08-891-845-10	Sequence 10, Appl
650	138.5	7.7	398	4	US-08-467-602-287	Sequence 287, App	723	135.5	7.5	501	3	US-09-514-845-10	Sequence 10, Appl
651	138.5	7.7	398	4	US-08-411-295F-213	Sequence 213, App	724	135.5	7.5	768	3	US-08-891-845-2	Sequence 2, Appl
652	138.5	7.7	409	4	US-08-467-602-284	Sequence 284, App	725	135.5	7.5	768	3	US-09-514-845-2	Sequence 2, Appl
653	138.5	7.7	409	4	US-08-411-295F-210	Sequence 210, App	726	135	7.5	492	3	US-08-462-794-11	Sequence 11, Appl
654	138.5	7.7	418	4	US-08-467-602-293	Sequence 293, App	727	135	7.5	497	4	US-09-499-846-6	Sequence 6, Appl
655	138.5	7.7	418	4	US-08-411-295F-219	Sequence 219, App	728	135	7.5	497	4	US-09-499-846-10	Sequence 10, Appl
656	138.5	7.7	569	4	US-08-467-602-237	Sequence 237, App	729	135	7.5	525	4	US-09-499-846-4	Sequence 4, Appl
657	138.5	7.7	569	4	US-08-411-295F-163	Sequence 163, App	730	135	7.5	525	4	US-09-499-846-8	Sequence 8, Appl
658	138.5	7.7	572	4	US-08-467-602-235	Sequence 235, App	731	134.5	7.4	349	3	US-08-470-335-188	Sequence 188, App

732	134.5	7.4	382	4	US-08-467-602-382	Sequence 382, App	805	134.5	7.4	889	4	US-08-411-295F-266	Sequence 266, App
733	134.5	7.4	434	3	US-09-540-245A-19	Sequence 19, App1	806	134.5	7.4	895	4	US-08-467-602-354	Sequence 354, App
734	134.5	7.4	456	3	US-08-470-335-246	Sequence 246, App	807	134.5	7.4	895	4	US-08-411-295F-280	Sequence 280, App
735	134.5	7.4	456	4	US-08-467-602-303	Sequence 303, App	808	134.5	7.4	898	4	US-08-467-602-351	Sequence 351, App
736	134.5	7.4	456	4	US-08-411-295F-229	Sequence 229, App	809	134.5	7.4	898	4	US-08-411-295F-277	Sequence 277, App
737	134.5	7.4	459	3	US-08-470-335-239	Sequence 239, App	810	134.5	7.4	899	3	US-08-470-335-249	Sequence 249, App
738	134.5	7.4	459	4	US-08-467-602-299	Sequence 299, App	811	134.5	7.4	899	4	US-08-467-602-301	Sequence 301, App
739	134.5	7.4	459	4	US-08-411-295F-225	Sequence 225, App	812	134.5	7.4	899	4	US-08-411-295F-227	Sequence 227, App
740	134.5	7.4	479	4	US-08-467-602-307	Sequence 307, App	813	134.5	7.4	902	3	US-08-470-335-242	Sequence 242, App
741	134.5	7.4	479	4	US-08-411-295F-233	Sequence 233, App	814	134.5	7.4	902	3	US-08-467-602-296	Sequence 296, App
742	134.5	7.4	490	4	US-08-467-602-345	Sequence 345, App	815	134.5	7.4	902	4	US-08-411-295F-222	Sequence 222, App
743	134.5	7.4	490	4	US-08-411-295F-271	Sequence 271, App	816	134.5	7.4	902	3	US-08-470-335-252	Sequence 252, App
744	134.5	7.4	493	4	US-08-467-602-341	Sequence 341, App	817	134.5	7.4	908	4	US-08-467-602-313	Sequence 313, App
745	134.5	7.4	493	4	US-08-411-295F-267	Sequence 267, App	818	134.5	7.4	908	4	US-08-411-295F-239	Sequence 239, App
746	134.5	7.4	513	4	US-08-467-602-349	Sequence 349, App	819	134.5	7.4	909	4	US-08-467-602-348	Sequence 348, App
747	134.5	7.4	513	4	US-08-411-295F-275	Sequence 275, App	820	134.5	7.4	909	4	US-08-411-295F-274	Sequence 274, App
748	134.5	7.4	526	1	US-08-471-570-4	Sequence 4, App1	821	134.5	7.4	911	3	US-08-470-335-245	Sequence 245, App
749	134.5	7.4	534	4	US-09-651-200-6	Sequence 6, App1	822	134.5	7.4	911	4	US-08-467-602-310	Sequence 310, App
750	134.5	7.4	534	4	US-09-651-200-24	Sequence 24, App1	823	134.5	7.4	911	4	US-08-411-295F-226	Sequence 226, App
751	134.5	7.4	635	3	US-08-470-335-247	Sequence 247, App	824	134.5	7.4	918	4	US-08-467-602-357	Sequence 357, App
752	134.5	7.4	635	4	US-08-467-602-302	Sequence 302, App	825	134.5	7.4	918	4	US-08-411-295F-283	Sequence 283, App
753	134.5	7.4	635	4	US-08-411-295F-228	Sequence 228, App	826	134.5	7.4	922	4	US-08-467-602-304	Sequence 304, App
754	134.5	7.4	638	3	US-08-470-335-240	Sequence 240, App	827	134.5	7.4	922	4	US-08-411-295F-230	Sequence 230, App
755	134.5	7.4	638	4	US-08-467-602-297	Sequence 297, App	828	134.5	7.4	931	4	US-08-467-602-316	Sequence 316, App
756	134.5	7.4	638	4	US-08-411-295F-223	Sequence 223, App	829	134.5	7.4	931	4	US-08-411-295F-242	Sequence 242, App
757	134.5	7.4	643	5	PCT-US93-00031-19	Sequence 19, App1	830	134.5	7.4	933	4	US-08-467-602-343	Sequence 343, App
758	134.5	7.4	644	3	US-08-470-335-250	Sequence 250, App	831	134.5	7.4	933	4	US-08-411-295F-269	Sequence 269, App
759	134.5	7.4	644	4	US-08-467-602-311	Sequence 311, App	832	134.5	7.4	936	4	US-08-467-602-338	Sequence 338, App
760	134.5	7.4	644	4	US-08-411-295F-237	Sequence 237, App	833	134.5	7.4	936	4	US-08-411-295F-264	Sequence 264, App
761	134.5	7.4	647	3	US-08-470-335-243	Sequence 243, App	834	134.5	7.4	942	4	US-08-467-602-355	Sequence 355, App
762	134.5	7.4	647	3	US-09-009-490A-91	Sequence 91, App	835	134.5	7.4	942	4	US-08-411-295F-281	Sequence 281, App
763	134.5	7.4	647	3	US-08-482-073-5	Sequence 5, App1	836	134.5	7.4	945	4	US-08-467-602-352	Sequence 352, App
764	134.5	7.4	647	4	US-08-467-602-308	Sequence 308, App	837	134.5	7.4	945	4	US-08-411-295F-278	Sequence 278, App
765	134.5	7.4	647	4	US-08-411-295F-234	Sequence 234, App	838	134.5	7.4	945	4	US-08-467-602-346	Sequence 346, App
766	134.5	7.4	647	5	PCT-US93-00031-11	Sequence 11, App1	839	134.5	7.4	956	4	US-08-411-295F-272	Sequence 272, App
767	134.5	7.4	647	5	PCT-US93-00031-23	Sequence 23, App1	840	134.5	7.4	956	4	US-08-467-602-358	Sequence 358, App
768	134.5	7.4	652	1	US-08-471-570-10	Sequence 10, App1	841	134.5	7.4	965	4	US-08-411-295F-284	Sequence 284, App
769	134.5	7.4	658	4	US-08-467-602-205	Sequence 205, App	842	134	7.4	965	4	US-08-411-295F-284	Sequence 284, App
770	134.5	7.4	658	4	US-08-411-295F-231	Sequence 231, App	843	134	7.4	424	6	5169835-6	Patent No. 5169835
771	134.5	7.4	667	4	US-08-467-602-314	Sequence 314, App	844	133.5	7.4	488	4	US-09-499-846-12	Sequence 12, App1
772	134.5	7.4	667	4	US-08-411-295F-240	Sequence 240, App	845	133.5	7.4	888	1	US-08-445-640-35	Sequence 35, App1
773	134.5	7.4	669	4	US-08-467-602-344	Sequence 344, App	846	133.5	7.4	888	3	US-08-170-558-35	Sequence 35, App1
774	134.5	7.4	669	4	US-08-411-295F-270	Sequence 270, App	847	133.5	7.4	888	3	US-08-447-314-35	Sequence 35, App1
775	134.5	7.4	672	4	US-08-467-602-339	Sequence 339, App	848	133.5	7.4	888	3	US-08-445-611-35	Sequence 35, App1
776	134.5	7.4	672	4	US-08-411-295F-265	Sequence 265, App	849	133.5	7.4	888	4	US-09-223-490-35	Sequence 35, App1
777	134.5	7.4	678	4	US-08-467-602-353	Sequence 353, App	850	133	7.4	317	4	US-09-684-708A-23	Sequence 23, App1
778	134.5	7.4	678	4	US-08-411-295F-279	Sequence 279, App	851	133	7.4	322	3	US-09-383-586-33	Sequence 33, App1
779	134.5	7.4	681	4	US-08-467-602-350	Sequence 350, App	852	133	7.4	322	4	US-09-823-038A-33	Sequence 33, App1
780	134.5	7.4	681	4	US-08-411-295F-276	Sequence 276, App	853	133	7.4	323	4	US-09-684-708A-25	Sequence 25, App1
781	134.5	7.4	692	4	US-08-467-602-347	Sequence 347, App	854	133	7.4	612	2	US-08-359-705B-8	Sequence 8, App1
782	134.5	7.4	692	4	US-08-411-295F-273	Sequence 273, App	855	133	7.4	612	2	US-08-286-846A-8	Sequence 8, App1
783	134.5	7.4	701	4	US-08-467-602-356	Sequence 356, App	856	133	7.4	612	3	US-08-457-880A-8	Sequence 8, App1
784	134.5	7.4	701	4	US-08-411-295F-282	Sequence 282, App	857	133	7.4	612	3	US-08-444-622A-8	Sequence 8, App1
785	134.5	7.4	740	5	PCT-US93-00031-17	Sequence 17, App1	858	133	7.4	612	3	US-08-942-562-8	Sequence 8, App1
786	134.5	7.4	852	3	US-08-470-335-248	Sequence 248, App	859	133	7.4	612	3	US-09-156-923-8	Sequence 8, App1
787	134.5	7.4	852	3	US-08-467-602-300	Sequence 300, App	860	133	7.4	816	4	US-09-949-016-10904	Sequence 10904, A
788	134.5	7.4	855	3	US-08-411-295F-226	Sequence 226, App	861	133	7.4	839	2	US-08-359-705B-6	Sequence 6, App1
789	134.5	7.4	855	3	US-08-470-335-241	Sequence 241, App	862	133	7.4	839	2	US-08-286-846A-6	Sequence 6, App1
790	134.5	7.4	855	4	US-08-467-602-298	Sequence 298, App	863	133	7.4	839	2	US-08-457-880A-6	Sequence 6, App1
791	134.5	7.4	855	4	US-08-411-295F-224	Sequence 224, App	864	133	7.4	839	3	US-08-444-622A-6	Sequence 6, App1
792	134.5	7.4	861	3	US-08-470-335-251	Sequence 251, App	865	133	7.4	839	3	US-08-942-562-6	Sequence 6, App1
793	134.5	7.4	861	4	US-08-467-602-312	Sequence 312, App	866	133	7.4	839	3	US-09-156-923-6	Sequence 6, App1
794	134.5	7.4	861	4	US-08-411-295F-238	Sequence 238, App	867	133	7.4	850	1	US-08-467-602-353	Sequence 7, App1
795	134.5	7.4	864	3	US-08-470-335-244	Sequence 244, App	868	133	7.4	850	2	US-08-441-104A-7	Sequence 7, App1
796	134.5	7.4	864	4	US-08-467-602-309	Sequence 309, App	869	133	7.4	850	2	US-08-440-816A-7	Sequence 7, App1
797	134.5	7.4	864	4	US-08-411-295F-235	Sequence 235, App	870	133	7.4	860	3	US-09-417-381A-7	Sequence 7, App1
798	134.5	7.4	875	4	US-08-467-602-306	Sequence 306, App	871	132	7.3	367	3	US-09-175-928-2	Sequence 2, App1
799	134.5	7.4	875	4	US-08-411-295F-232	Sequence 232, App	872	132	7.3	408	3	US-09-1724-864-62	Sequence 62, App1
800	134.5	7.4	884	4	US-08-467-602-315	Sequence 315, App	873	131.5	7.3	312	4	US-09-254-465A-9	Sequence 9, App1
801	134.5	7.4	884	4	US-08-411-295F-241	Sequence 241, App	883	131.5	7.3	312	4	US-09-353-469-9	Sequence 9, App1
802	134.5	7.4	886	4	US-08-467-602-342	Sequence 342, App	884	131	7.3	240	1	US-08-471-570-12	Sequence 12, App1
803	134.5	7.4	886	4	US-08-411-295F-268	Sequence 268, App	885	131	7.3	320	1	US-09-684-708A-27	Sequence 27, App1
804	134.5	7.4	889	4	US-08-467-602-340	Sequence 340, App	886	131	7.3	561	4	US-09-866-510-24	Sequence 24, App1

887	131	7.3	782	4	US-09-684-708A-21	Sequence 21, Appl	960	127	7.0	992	4	US-09-872-136B-2	Sequence 2, Appl
888	131	7.3	1090	1	US-09-866-510-14	Sequence 14, Appl	961	127	7.0	992	5	PCT-US93-02750-2	Sequence 2, Appl
889	131	7.3	1106	4	US-08-180-195-2	Sequence 2, Appl	962	127	7.0	992	5	PCT-US93-05401-2	Sequence 2, Appl
890	131	7.3	1106	1	US-08-168-917-2	Sequence 2, Appl	963	127	7.0	992	5	PCT-US93-09893-2	Sequence 2, Appl
891	131	7.3	1106	1	US-08-477-329-2	Sequence 2, Appl	964	126.5	7.0	365	2	US-09-979-424-3	Sequence 2, Appl
892	131	7.3	1106	1	US-08-475-458-2	Sequence 2, Appl	965	126.5	7.0	365	3	US-09-272-496-2	Sequence 2, Appl
893	131	7.3	1106	2	US-08-460-510-2	Sequence 2, Appl	966	126.5	7.0	365	3	US-09-272-496-2	Sequence 2, Appl
894	131	7.3	1106	2	US-08-460-490-2	Sequence 2, Appl	967	126	7.0	365	4	US-09-949-016-6064	Sequence 6064, Ap
895	131	7.3	1106	3	US-08-980-400-2	Sequence 2, Appl	968	126	7.0	477	2	US-08-359-705B-4	Sequence 3, Appl
896	131	7.3	1106	3	US-08-462-728-4	Sequence 2, Appl	969	126	7.0	477	2	US-08-286-846A-4	Sequence 4, Appl
897	131	7.3	1106	3	US-09-583-459A-2	Sequence 2, Appl	970	126	7.0	477	2	US-08-457-880A-4	Sequence 4, Appl
898	131	7.3	1106	3	US-09-583-210-2	Sequence 2, Appl	971	126	7.0	477	3	US-08-444-622A-4	Sequence 4, Appl
899	131	7.3	1106	3	US-09-583-449A-2	Sequence 2, Appl	972	126	7.0	477	3	US-08-942-562-4	Sequence 4, Appl
900	131	7.3	1106	3	US-09-435-059-2	Sequence 2, Appl	973	126	7.0	477	3	US-09-156-923-4	Sequence 4, Appl
901	131	7.3	1106	3	US-08-461-917-4	Sequence 2, Appl	974	126	7.0	822	2	US-08-359-705B-2	Sequence 2, Appl
902	131	7.3	1106	4	US-08-464-436-4	Sequence 4, Appl	975	126	7.0	822	2	US-08-286-846A-2	Sequence 2, Appl
903	131	7.3	1106	4	US-08-464-436-4	Sequence 4, Appl	976	126	7.0	822	2	US-08-457-880A-2	Sequence 2, Appl
904	131	7.3	1106	4	US-09-866-510-16	Sequence 16, Appl	977	126	7.0	822	3	US-08-444-622A-2	Sequence 2, Appl
905	131	7.3	1106	4	US-09-866-510-18	Sequence 18, Appl	978	126	7.0	822	3	US-08-942-562-2	Sequence 2, Appl
906	131	7.3	1106	4	US-09-866-510-20	Sequence 20, Appl	979	126	7.0	822	3	US-09-156-923-2	Sequence 2, Appl
907	131	7.3	1106	4	US-09-866-510-22	Sequence 22, Appl	980	126	7.0	822	4	US-09-949-016-6698	Sequence 6698, Ap
908	131	7.3	1106	5	PCT-US92-00730-2	Sequence 2, Appl	981	126	7.0	847	1	US-08-286-105A-5	Sequence 5, Appl
909	131	7.3	1106	5	PCT-US92-00862-2	Sequence 2, Appl	982	126	7.0	847	2	US-08-441-104A-5	Sequence 5, Appl
910	130.5	7.2	298	4	US-09-152-060-76	Sequence 76, Appl	983	126	7.0	847	2	US-08-440-816A-5	Sequence 5, Appl
911	130.5	7.2	315	4	US-09-949-016-11121	Sequence 11121, A	984	126	7.0	1000	1	US-08-417-381A-5	Sequence 2, Appl
912	130.5	7.2	315	4	US-09-949-016-11122	Sequence 11122, A	985	126	7.0	1000	1	US-08-222-299-2	Sequence 2, Appl
913	130.5	7.2	432	3	US-08-477-460B-2	Sequence 2, Appl	986	126	7.0	1000	2	US-08-434-878-2	Sequence 2, Appl
914	130.5	7.2	432	3	US-08-379-516-2	Sequence 2, Appl	987	126	7.0	1000	5	PCT-US93-03718-2	Sequence 2, Appl
915	130.5	7.2	432	3	US-09-329-916-2	Sequence 2, Appl	988	125.5	6.9	365	3	US-08-928-383B-2	Sequence 2, Appl
916	130.5	7.2	432	3	US-08-485-312A-2	Sequence 2, Appl	989	125.5	6.9	518	4	US-09-919-172-20	Sequence 20, Appl
917	130.5	7.2	432	3	US-09-409-006A-2	Sequence 2, Appl	990	125.5	6.9	526	4	US-09-910-174B-9	Sequence 9, Appl
918	130.5	7.2	432	4	US-08-484-681-2	Sequence 2, Appl	991	125.5	6.9	526	4	US-09-620-461-9	Sequence 9, Appl
919	130.5	7.2	432	4	US-09-766-995-2	Sequence 2, Appl	992	125.5	6.9	526	4	US-09-949-016-6122	Sequence 6122, Ap
920	130.5	7.2	432	5	PCT-US93-07422-2	Sequence 2, Appl	993	125.5	6.9	540	4	US-09-949-016-11644	Sequence 11644, A
921	130.5	7.2	466	4	US-09-604-107A-8	Sequence 8, Appl	994	125.5	6.9	589	2	US-08-724-394A-1	Sequence 1, Appl
922	130	7.2	249	4	US-09-336-536-42	Sequence 42, Appl	995	125	6.9	391	5	PCT-US93-15696-2	Sequence 54, Appl
923	130	7.2	394	4	US-09-336-536-39	Sequence 39, Appl	996	124.5	6.9	241	3	US-08-341-018-54	Sequence 54, Appl
924	130	7.2	802	1	US-07-912-952-4	Sequence 33, Appl	997	124.5	6.9	241	3	US-08-470-339-195	Sequence 195, App
925	129.5	7.2	728	3	US-09-173-151A-33	Sequence 4, Appl	998	124.5	6.9	241	3	US-08-470-339-195	Sequence 195, App
926	129	7.1	340	3	US-09-188-930-184	Sequence 184, App	999	124.5	6.9	241	4	US-08-457-602-389	Sequence 389, App
927	129	7.1	340	4	US-09-312-283C-184	Sequence 184, App	1000	124.5	6.9	241	4	US-08-411-295F-47	Sequence 47, Appl
928	129	7.1	417	4	US-09-949-016-6729	Sequence 6729, App	1001	124.5	6.9	731	1	US-08-070-165F-10	Sequence 10, Appl
929	129	7.1	456	4	US-09-949-016-7564	Sequence 7564, Ap	1002	124.5	6.9	731	2	US-08-885-418-10	Sequence 10, Appl
930	128	7.1	341	4	US-09-336-536-29	Sequence 29, Appl	1003	124	6.9	198	4	US-09-569-611C-34	Sequence 34, Appl
931	128	7.1	370	4	US-09-336-536-28	Sequence 28, Appl	1004	124	6.9	637	4	US-09-569-611C-35	Sequence 35, Appl
932	128	7.1	483	2	US-08-392-338A-19	Sequence 19, Appl	1005	124	6.9	993	1	US-07-977-451-4	Sequence 4, Appl
933	128	7.1	483	3	US-09-166-750-19	Sequence 19, Appl	1006	124	6.9	993	1	US-08-252-517-4	Sequence 4, Appl
934	128	7.1	483	3	US-09-166-093-19	Sequence 19, Appl	1007	124	6.9	993	1	US-07-906-397A-4	Sequence 4, Appl
935	128	7.1	483	3	US-09-172-019-19	Sequence 19, Appl	1008	124	6.9	993	1	US-08-601-891-4	Sequence 4, Appl
936	128	7.1	483	3	US-09-166-094-19	Sequence 19, Appl	1009	124	6.9	993	2	US-09-021-324-4	Sequence 4, Appl
937	128	7.1	483	4	US-09-443-213-19	Sequence 19, Appl	1010	124	6.9	993	4	US-09-872-136B-4	Sequence 4, Appl
938	128	7.1	483	4	US-09-949-016-8574	Sequence 8574, Ap	1011	124	6.9	993	5	PCT-US92-09893-4	Sequence 4, Appl
939	128	7.1	795	4	US-09-949-016-7119	Sequence 7119, Ap	1012	124	6.9	999	1	US-08-252-626A-2	Sequence 2, Appl
940	128	7.1	806	3	US-09-383-630-3	Sequence 3, Appl	1013	124	6.9	999	1	US-09-949-016-6718	Sequence 6718, Ap
941	127.5	7.1	100	4	US-08-411-295F-121	Sequence 121, App	1014	124	6.9	1160	5	PCT-US92-05401-81	Sequence 4, Appl
942	127.5	7.1	206	3	US-08-341-018-2	Sequence 2, Appl	1015	123.5	6.8	156	4	US-08-467-602-306	Sequence 306, App
943	127.5	7.1	206	3	US-08-470-335-190	Sequence 190, App	1016	123.5	6.8	156	4	US-08-411-295F-306	Sequence 306, App
944	127.5	7.1	206	3	US-08-470-339-190	Sequence 190, App	1017	123.5	6.8	241	1	US-07-847-743B-30	Sequence 30, Appl
945	127.5	7.1	206	3	US-08-467-602-383	Sequence 383, App	1018	123.5	6.8	241	1	US-08-456-201-30	Sequence 30, Appl
946	127.5	7.1	206	4	US-08-411-295F-2	Sequence 2, Appl	1019	123.5	6.8	241	1	US-08-456-241-30	Sequence 30, Appl
947	127.5	7.1	206	4	US-08-411-295F-76	Sequence 76, Appl	1020	123.5	6.8	241	5	PCT-US92-04295A-30	Sequence 30, Appl
948	127.5	7.1	241	4	US-08-411-295F-94	Sequence 94, Appl	1021	123.5	6.8	420	1	US-07-847-743B-29	Sequence 29, Appl
949	127.5	7.1	431	3	US-09-038-832-2	Sequence 2, Appl	1022	123.5	6.8	420	1	US-08-456-201-29	Sequence 29, Appl
950	127.5	7.1	431	3	US-09-038-832-4	Sequence 4, Appl	1023	123.5	6.8	420	2	US-08-456-241-29	Sequence 29, Appl
951	127.5	7.1	447	4	US-09-949-016-8211	Sequence 8211, Ap	1024	123.5	6.8	420	5	PCT-US92-04295A-29	Sequence 29, Appl
952	127	7.0	383	4	US-09-949-016-11050	Sequence 11050, A	1025	123.5	6.8	637	1	US-07-847-743B-28	Sequence 28, Appl
953	127	7.0	992	1	US-07-813-593-2	Sequence 2, Appl	1026	123.5	6.8	637	1	US-08-456-201-28	Sequence 28, Appl
954	127	7.0	992	1	US-07-977-451-2	Sequence 2, Appl	1027	123.5	6.8	637	2	US-08-456-241-28	Sequence 28, Appl
955	127	7.0	992	1	US-07-946-507-2	Sequence 2, Appl	1028	123.5	6.8	637	5	PCT-US92-04295A-28	Sequence 28, Appl
956	127	7.0	992	1	US-08-252-517-2	Sequence 2, Appl	1029	123.5	6.8	645	1	US-07-847-743B-27	Sequence 27, Appl
957	127	7.0	992	1	US-07-906-387A-2	Sequence 2, Appl	1030	123.5	6.8	645	1	US-08-456-201-27	Sequence 27, Appl
958	127	7.0	992	1	US-08-601-891-2	Sequence 2, Appl	1031	123.5	6.8	645	1	US-08-428-526-4	Sequence 4, Appl
959	127	7.0	992	2	US-09-021-324-2	Sequence 2, Appl	1032	123.5	6.8	645	1	US-08-428-927-4	Sequence 4, Appl

1033	123.5	6.8	645	1	US-08-428-298-4	Sequence 4, Appli	1106	122.5	6.8	626	4	US-08-411-295F-148	Sequence 148, App
1034	123.5	6.8	645	1	US-08-339-517-4	Sequence 27, Appli	1107	122.5	6.8	635	4	US-08-467-602-231	Sequence 231, App
1035	123.5	6.8	645	2	US-08-456-241-27	Sequence 27, Appli	1108	122.5	6.8	635	4	US-08-411-295F-157	Sequence 157, App
1036	123.5	6.8	645	3	US-09-020-880-93	Sequence 93, Appli	1109	122.5	6.8	637	4	US-08-467-602-258	Sequence 258, App
1037	123.5	6.8	645	3	US-09-101-544-93	Sequence 93, Appli	1110	122.5	6.8	637	4	US-08-411-295F-184	Sequence 184, App
1038	123.5	6.8	645	4	US-09-097-681-3	Sequence 3, Appli	1111	122.5	6.8	640	4	US-08-467-602-256	Sequence 256, App
1039	123.5	6.8	645	5	PCT-US92-04295A-27	Sequence 27, Appli	1112	122.5	6.8	640	4	US-08-411-295F-182	Sequence 182, App
1040	123.5	6.8	732	1	US-07-847-743B-9	Sequence 9, Appli	1113	122.5	6.8	645	3	US-08-753-007A-10	Sequence 10, Appli
1041	123.5	6.8	732	1	US-08-456-201-9	Sequence 9, Appli	1114	122.5	6.8	645	3	US-09-398-496-10	Sequence 10, Appli
1042	123.5	6.8	732	2	US-08-456-241-9	Sequence 9, Appli	1115	122.5	6.8	646	4	US-08-467-602-210	Sequence 210, App
1043	123.5	6.8	732	2	PCT-US92-04295A-9	Sequence 9, Appli	1116	122.5	6.8	646	4	US-08-411-295F-196	Sequence 196, App
1044	123.5	6.8	732	4	US-09-254-465A-2	Sequence 2, Appli	1117	122.5	6.8	649	4	US-08-467-602-267	Sequence 267, App
1045	123	6.8	321	4	US-09-953-499-2	Sequence 2, Appli	1118	122.5	6.8	649	4	US-08-411-295F-193	Sequence 193, App
1046	123	6.8	354	6	5169835-4	Patent No. 5169835	1119	122.5	6.8	650	4	US-08-467-602-217	Sequence 217, App
1047	123	6.8	354	6	5169835-4	Patent No. 5169835	1120	122.5	6.8	650	4	US-08-411-295F-143	Sequence 143, App
1048	123	6.8	553	3	US-09-173-151A-35	Sequence 9, Appli	1121	122.5	6.8	653	4	US-08-467-602-212	Sequence 212, App
1049	123	6.8	668	3	US-08-339-578-2	Sequence 35, Appli	1122	122.5	6.8	653	4	US-08-411-295F-138	Sequence 138, App
1050	123	6.8	821	1	US-08-467-602-380	Sequence 2, Appli	1123	122.5	6.8	659	4	US-08-467-602-229	Sequence 229, App
1051	122.5	6.8	133	4	US-08-467-602-130	Sequence 380, App	1124	122.5	6.8	659	4	US-08-411-295F-155	Sequence 155, App
1052	122.5	6.8	161	1	US-08-096-277-18	Sequence 18, App	1125	122.5	6.8	659	4	US-08-467-602-264	Sequence 264, App
1053	122.5	6.8	161	2	US-08-550-815-18	Sequence 18, App	1126	122.5	6.8	660	4	US-08-411-295F-190	Sequence 190, App
1054	122.5	6.8	161	3	US-08-703-089-18	Sequence 18, Appli	1127	122.5	6.8	662	4	US-08-467-602-226	Sequence 226, App
1055	122.5	6.8	207	4	US-08-467-602-219	Sequence 18, Appli	1128	122.5	6.8	662	4	US-08-411-295F-152	Sequence 152, App
1056	122.5	6.8	207	4	US-08-467-602-219	Sequence 18, App	1129	122.5	6.8	662	4	US-07-847-743B-8	Sequence 8, Appli
1057	122.5	6.8	210	4	US-08-467-602-215	Sequence 215, App	1130	122.5	6.8	669	1	US-07-847-743B-13	Sequence 13, Appli
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1061	122.5	6.8	241	4	US-08-467-602-261	Sequence 261, App	1134	122.5	6.8	669	2	US-08-456-241-8	Sequence 8, Appli
1062	122.5	6.8	241	4	US-08-411-295F-187	Sequence 187, App	1135	122.5	6.8	669	2	US-08-456-240-13	Sequence 13, Appli
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1064	122.5	6.8	244	4	US-08-411-295F-183	Sequence 183, App	1137	122.5	6.8	669	2	US-08-419-878B-11	Sequence 11, Appli
1065	122.5	6.8	264	4	US-08-467-602-265	Sequence 265, App	1138	122.5	6.8	669	3	US-09-173-480-11	Sequence 11, Appli
1066	122.5	6.8	264	4	US-08-411-295F-191	Sequence 191, App	1139	122.5	6.8	669	3	US-08-467-602-273	Sequence 273, App
1067	122.5	6.8	386	4	US-08-467-602-218	Sequence 218, App	1140	122.5	6.8	669	4	US-08-411-295F-199	Sequence 199, App
1068	122.5	6.8	386	4	US-08-411-295F-144	Sequence 144, App	1141	122.5	6.8	669	5	PCT-US92-04295A-8	Sequence 8, Appli
1069	122.5	6.8	389	4	US-08-467-602-213	Sequence 213, App	1142	122.5	6.8	669	5	PCT-US92-04295A-13	Sequence 13, Appli
1070	122.5	6.8	389	4	US-08-411-295F-139	Sequence 139, App	1143	122.5	6.8	673	4	US-08-467-602-220	Sequence 220, App
1071	122.5	6.8	395	4	US-08-467-602-227	Sequence 227, App	1144	122.5	6.8	673	4	US-08-411-295F-146	Sequence 146, App
1072	122.5	6.8	395	4	US-08-411-295F-153	Sequence 153, App	1145	122.5	6.8	682	4	US-08-467-602-232	Sequence 232, App
1073	122.5	6.8	398	4	US-08-467-602-224	Sequence 224, App	1146	122.5	6.8	682	4	US-08-411-295F-158	Sequence 158, App
1074	122.5	6.8	398	4	US-08-411-295F-150	Sequence 150, App	1147	122.5	6.8	684	4	US-08-467-602-259	Sequence 259, App
1075	122.5	6.8	409	4	US-08-467-602-221	Sequence 221, App	1148	122.5	6.8	684	4	US-08-411-295F-185	Sequence 185, App
1076	122.5	6.8	409	4	US-08-411-295F-147	Sequence 147, App	1149	122.5	6.8	687	4	US-08-467-602-254	Sequence 254, App
1077	122.5	6.8	418	4	US-08-467-602-230	Sequence 230, App	1150	122.5	6.8	687	4	US-08-411-295F-180	Sequence 180, App
1078	122.5	6.8	418	4	US-08-411-295F-156	Sequence 156, App	1151	122.5	6.8	693	4	US-08-467-602-271	Sequence 271, App
1079	122.5	6.8	420	4	US-08-467-602-260	Sequence 260, App	1152	122.5	6.8	693	4	US-08-411-295F-197	Sequence 197, App
1080	122.5	6.8	420	4	US-08-411-295F-186	Sequence 186, App	1153	122.5	6.8	696	4	US-08-467-602-268	Sequence 268, App
1081	122.5	6.8	422	3	US-08-753-007A-9	Sequence 9, Appli	1154	122.5	6.8	696	4	US-08-411-295F-194	Sequence 194, App
1082	122.5	6.8	422	3	US-09-398-496-9	Sequence 9, Appli	1155	122.5	6.8	707	4	US-08-467-602-262	Sequence 262, App
1083	122.5	6.8	423	3	US-08-467-602-255	Sequence 255, App	1156	122.5	6.8	707	4	US-08-411-295F-188	Sequence 188, App
1084	122.5	6.8	423	4	US-08-411-295F-181	Sequence 181, App	1157	122.5	6.8	716	4	US-08-467-602-274	Sequence 274, App
1085	122.5	6.8	429	4	US-08-467-602-269	Sequence 269, App	1158	122.5	6.8	716	4	US-08-411-295F-200	Sequence 200, App
1086	122.5	6.8	429	4	US-08-411-295F-195	Sequence 195, App	1159	122	6.8	146	4	US-09-270-767-33187	Sequence 33187, A
1087	122.5	6.8	432	4	US-08-467-602-266	Sequence 266, App	1160	122	6.8	357	4	US-09-949-016-9974	Sequence 9074, App
1088	122.5	6.8	432	4	US-08-411-295F-192	Sequence 192, App	1161	122	6.8	357	4	US-09-949-016-11040	Sequence 11040, App
1089	122.5	6.8	443	4	US-08-467-602-263	Sequence 263, App	1162	122	6.8	647	3	US-08-753-007A-32	Sequence 32, Appli
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1092	122.5	6.8	452	4	US-08-411-295F-198	Sequence 198, App	1165	122	6.8	649	3	US-08-168-091A-4618	Sequence 4618, A
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1096	122.5	6.8	606	4	US-08-411-295F-140	Sequence 140, App	1169	121.5	6.7	302	2	US-08-979-424-1	Sequence 1, Appli
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1098	122.5	6.8	612	4	US-08-411-295F-154	Sequence 154, App	1171	121.5	6.7	302	2	US-08-441-944A-7	Sequence 7, Appli
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1191	120	6.6	205	3	US-09-462-270-4	Sequence 4, Appli	1282	116.5	6.5	315	2	US-08-332-562A-83	Sequence 83, Appli
1192	120	6.6	328	4	US-09-949-016-6428	Sequence 6428, Ap	1283	116.5	6.5	315	4	US-09-949-016-7014	Sequence 7014, Ap
1193	120	6.6	329	4	US-09-149-476-483	Sequence 483, App	1284	116.5	6.5	680	3	US-08-227-496C-15	Sequence 15, Appli
1194	120	6.6	361	4	US-09-949-016-7327	Sequence 7327, Ap	1285	116.5	6.5	1060	3	US-09-419-788-19	Sequence 19, Appli
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1207	119.5	6.6	477	4	US-09-949-016-9192	Sequence 9192, Ap	1289	116	6.4	731	3	US-08-439-992A-3	Sequence 3, Appli
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1211	119.5	6.6	477	4	US-09-949-016-9196	Sequence 9196, Ap	1293	115.5	6.4	173	3	US-08-833-488B-31	Sequence 31, Appli
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1228	118	6.5	933	3	US-08-222-299-4	Sequence 4, Appli	1310	114.5	6.3	365	3	US-09-046-736-2	Sequence 2, Appli
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1239	117.5	6.5	569	1	US-07-821-716-2	Sequence 2, Appli	1321	113.5	6.3	307	4	US-09-556-972-21	Sequence 21, Appli
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1242	117.5	6.5	569	3	US-08-685-212-2	Sequence 2, Appli	1324	113.5	6.3	518	3	US-09-591-435-8	Sequence 8, Appli
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1245	117.5	6.5	569	4	US-08-406-824A-6	Sequence 6, Appli	1327	113.5	6.3	537	1	US-08-604-333-4	Sequence 4, Appli
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1247	117.5	6.5	569	5	PCT-US94-02414-2	Sequence 2, Appli	1329	113.5	6.3	537	4	US-09-173-151A-29	Sequence 29, Appli
1248	117.5	6.5	569	5	PCT-US96-08899-2	Sequence 2, Appli	1330	113.5	6.3	537	4	US-09-578-178-4	Sequence 4, Appli
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1252	117	6.5	407	3	US-08-753-007A-6	Sequence 6, Appli	1334	113.5	6.3	273	4	US-09-270-767-32843	Sequence 32843, A
1253	117	6.5	708	3	US-09-398-486-6	Sequence 6, Appli	1335	113	6.3	273	4	US-09-270-767-48060	Sequence 48060, A
1254	117	6.5	729	1	US-07-640-029-3	Sequence 3, Appli	1336	113	6.3	278	4	US-09-270-767-48060	Sequence 48060, A
1255	117	6.5	729	1	US-07-640-029-3	Sequence 3, Appli	1337	113	6.3	458	4	US-09-773-877B-22	Sequence 22, Appli
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1258	117	6.5	733	3	US-08-441-944A-6	Sequence 6, Appli	1340	112.5	6.2	181	4	US-09-858-664A-13	Sequence 13, Appli
1259	117	6.5	733	3	US-08-439-992A-4	Sequence 4, Appli	1341	112.5	6.2	181	4	US-10-274-978-14	Sequence 14, Appli
1260	117	6.5	825	1	US-07-912-952-2	Sequence 2, Appli	1342	112.5	6.2	414	4	US-10-697-263-14	Sequence 14, Appli
1261	117	6.5	885	1	US-08-372-892-4	Sequence 4, Appli	1343	112.5	6.2	503	4	US-08-999-689A-6	Sequence 6, Appli
1262	117	6.5	885	1	US-08-372-892-4	Sequence 4, Appli	1344	112.5	6.2	503	4	US-09-944-807-4	Sequence 4, Appli
1263	117	6.5	894	1	US-08-372-892-2	Sequence 2, Appli	1345	112	6.2	170	4	US-09-245-764-6	Sequence 6, Appli
1264	117	6.5	894	1	US-08-445-640-34	Sequence 34, Appli	1346	112	6.2	181	3	US-08-753-007A-4	Sequence 4, Appli
1265	117	6.5	894	3	US-08-170-558-34	Sequence 34, Appli	1347	112	6.2	247	6	US-09-398-496-4	Sequence 4, Appli
1266	117	6.5	894	3	US-08-447-314-34	Sequence 34, Appli	1348	112	6.2	247	6	5455030-9	Patent No. 5455030
1267	117	6.5	894	3	US-08-445-461-34	Sequence 34, Appli	1349	112	6.2	605	3	US-08-753-007A-2	Sequence 2, Appli
1268	117	6.5	894	3	US-09-223-490-34	Sequence 34, Appli	1350	112	6.2	605	3	US-09-398-496-2	Sequence 2, Appli
1269	117	6.5	975	4	US-09-949-016-7595	Sequence 7595, Ap	1351	112	6.2	605	3	US-09-398-496-2	Sequence 2, Appli

1352	111.5	6.2	94	US-08-341-843B-30	Sequence 30, Appl
1353	111.5	6.2	94	US-08-427-497B-35	Sequence 35, Appl
1354	111.5	6.2	284	US-08-961-309-70	Sequence 70, Appl
1355	111.5	6.2	431	US-09-773-877B-27	Sequence 27, Appl
1356	111.5	6.2	468	US-09-773-877B-26	Sequence 26, Appl
1357	111.5	6.2	480	US-08-425-889B-11	Sequence 11, Appl
1358	111.5	6.2	567	US-09-560-639-7	Sequence 7, Appl
1359	111.5	6.2	567	US-09-173-151A-24	Sequence 24, Appl
1360	111.5	6.2	567	US-09-032-337-39	Sequence 39, Appl
1361	111	6.1	275	US-08-463-903-6	Sequence 6, Appl
1362	111	6.1	275	US-08-463-903-8	Sequence 8, Appl
1363	111	6.1	275	US-07-935-695-6	Sequence 6, Appl
1364	111	6.1	275	US-07-935-695-8	Sequence 8, Appl
1365	111	6.1	280	US-08-463-903-10	Sequence 10, Appl
1366	111	6.1	280	US-07-935-695-10	Sequence 10, Appl
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1368	111	6.1	282	US-07-935-695-12	Sequence 12, Appl
1369	111	6.1	321	US-09-361-434-17	Sequence 17, Appl
1370	111	6.1	321	US-09-361-434-12	Sequence 22, Appl
1371	111	6.1	321	US-09-635-025-17	Sequence 17, Appl
1372	111	6.1	321	US-09-635-025-22	Sequence 22, Appl
1373	111	6.1	398	US-08-091-519-2	Sequence 2, Appl
1374	111	6.1	398	US-08-442-043A-2	Sequence 2, Appl
1375	111	6.1	398	US-09-173-151A-26	Sequence 26, Appl
1376	111	6.1	398	US-09-461-508-2	Sequence 2, Appl
1377	111	6.1	398	US-08-441-893A-2	Sequence 2, Appl
1378	111	6.1	398	US-09-579-845-4	Sequence 4, Appl
1379	111	6.1	398	US-08-406-824A-8	Sequence 8, Appl
1380	111	6.1	398	US-09-921-667-8	Sequence 8, Appl
1381	111	6.1	398	PCT-US91-03478-2	Sequence 2, Appl
1382	111	6.1	418	US-09-949-016-945B	Sequence 945B, Ap
1383	111	6.1	467	US-08-030-175-41	Sequence 41, Appl
1384	111	6.1	467	US-08-030-175-42	Sequence 42, Appl
1385	111	6.1	479	US-09-723-368-2	Sequence 2, Appl
1386	111	6.1	479	US-09-949-016-627B	Sequence 627B, Ap
1387	111	6.1	522	US-09-949-016-563	Sequence 563, Ap
1388	111	6.1	521	US-08-896-537A-2	Sequence 2, Appl
1389	111	6.1	729	US-08-070-165F-6	Sequence 6, Appl
1390	111	6.1	729	US-08-885-418-6	Sequence 6, Appl
1391	110.5	6.1	141	US-09-858-664A-15	Sequence 15, Appl
1392	110.5	6.1	141	US-10-274-978-16	Sequence 16, Appl
1393	110.5	6.1	141	US-10-697-263-16	Sequence 16, Appl
1394	110.5	6.1	260	US-08-463-903-2	Sequence 2, Appl
1395	110.5	6.1	260	US-07-935-695-2	Sequence 2, Appl
1396	110.5	6.1	260	US-08-961-309-64	Sequence 64, Appl
1397	110.5	6.1	275	US-08-463-903-17	Sequence 17, Appl
1398	110.5	6.1	275	US-07-935-695-17	Sequence 17, Appl
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1400	110.5	6.1	584	US-09-620-461-16	Sequence 16, Appl
1401	110.5	6.1	601	US-08-795-868-16	Sequence 16, Appl
1402	110.5	6.1	602	US-09-303-069-16	Sequence 16, Appl
1403	110.5	6.1	602	US-09-134-250-16	Sequence 16, Appl
1404	110.5	6.1	602	US-08-224-591-14	Sequence 14, Appl
1405	110.5	6.1	242	US-08-382-338A-23	Sequence 22, Appl
1406	110	6.1	242	US-08-926-789-14	Sequence 14, Appl
1407	110	6.1	242	US-09-166-750-23	Sequence 23, Appl
1408	110	6.1	242	US-09-166-093-23	Sequence 23, Appl
1409	110	6.1	242	US-09-172-019-23	Sequence 23, Appl
1410	110	6.1	242	US-09-166-094-23	Sequence 23, Appl
1411	110	6.1	244	US-09-443-213-23	Sequence 23, Appl
1412	110	6.1	244	PCT-US93-11138-14	Sequence 14, Appl
1413	110	6.1	547	US-08-314-615-1	Sequence 1, Appl
1414	110	6.1	547	US-08-433-010-1	Sequence 1, Appl
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1431	110	6.1	547	US-08-482-882-1	Sequence 1, Appl
1432	110	6.1	547	US-08-482-882-1	Sequence 1, Appl
1433	110	6.1	547	US-08-482-882-1	Sequence 1, Appl

RESULT 1

1434	110	6.1	547	US-08-296-749-1	Sequence 1, Appl
1435	110	6.1	547	US-08-314-369-1	Sequence 1, Appl
1436	110	6.1	771	US-08-434-000A-8	Sequence 8, Appl
1437	110	6.1	771	US-09-112-157-8	Sequence 8, Appl
1438	110	6.1	771	US-09-717-888-8	Sequence 8, Appl
1439	109.5	6.1	274	US-08-961-309-66	Sequence 66, Appl
1440	109.5	6.1	453	5284931-3	Patent No. 5284931
1441	109.5	6.1	453	5284931-3	Patent No. 5284931
1442	109.5	6.1	505	US-08-318-039A-1	Sequence 1, Appl
1443	109.5	6.1	505	US-08-318-038B-15	Sequence 15, Appl
1444	109.5	6.1	505	US-08-227-496C-19	Sequence 19, Appl
1445	109.5	6.1	505	US-08-435-568A-1	Sequence 1, Appl
1446	109.5	6.1	505	US-09-240-915-6	Sequence 6, Appl
1447	109.5	6.1	505	US-09-591-435-6	Sequence 6, Appl
1448	109.5	6.1	507	US-08-464-083-14	Sequence 14, Appl
1449	109.5	6.1	507	US-08-469-587B-14	Sequence 14, Appl
1450	109.5	6.1	531	US-08-789-078-3	Sequence 3, Appl
1451	109.5	6.1	531	US-08-752-633-3	Sequence 3, Appl
1452	109.5	6.1	531	PCT-US95-04886-3	Sequence 3, Appl
1453	109.5	6.1	532	US-07-618-286-1	Sequence 1, Appl
1454	109.5	6.1	532	US-08-483-389-118	Sequence 118, App
1455	109.5	6.1	532	US-08-689-870-12	Sequence 12, Appl
1456	109.5	6.1	532	US-09-009-490A-87	Sequence 87, Appl
1457	109.5	6.1	532	5284931-2	Patent No. 5284931
1458	109.5	6.1	532	5284931-2	Patent No. 5284931
1459	109	6.0	170	US-09-270-767-43106	Sequence 43106, A
1460	109	6.0	282	US-08-463-903-15	Sequence 15, Appl
1461	109	6.0	282	US-07-935-695-15	Sequence 15, Appl
1462	109	6.0	285	US-08-463-903-22	Sequence 22, Appl
1463	109	6.0	285	US-07-935-695-22	Sequence 22, Appl
1464	109	6.0	488	US-09-517-605-3	Sequence 3, Appl
1465	109	6.0	1140	US-09-579-692B-8	Sequence 8, Appl
1466	108	6.0	329	US-10-000-489-78	Sequence 78, Appl
1467	108	6.0	329	US-09-910-174A-12	Sequence 12, Appl
1468	108	6.0	319	US-09-620-461-12	Sequence 12, Appl
1469	108	6.0	474	US-09-828-995B-17	Sequence 17, Appl
1470	107.5	6.0	199	US-08-768-964-12	Sequence 12, Appl
1471	107.5	6.0	199	US-09-005-299-12	Sequence 12, Appl
1472	107.5	6.0	199	US-09-515-431-12	Sequence 12, Appl
1473	107.5	6.0	263	US-08-768-964-2	Sequence 2, Appl
1474	107.5	6.0	263	US-09-005-299-2	Sequence 2, Appl
1475	107.5	6.0	263	US-09-515-431-12	Sequence 2, Appl
1476	107.5	6.0	264	US-08-323-445A-8	Sequence 8, Appl
1477	107.5	6.0	264	US-08-515-903A-8	Sequence 8, Appl
1478	107.5	6.0	264	PCT-US95-1284A-8	Sequence 8, Appl
1479	107.5	5.9	318	US-09-656-952-2	Sequence 2, Appl
1480	107	5.9	344	US-09-656-952-19	Sequence 19, Appl
1481	107	5.9	344	US-09-656-952-20	Sequence 20, Appl
1482	106.5	5.9	248	5455030-11	Patent No. 5455030
1483	106.5	5.9	248	5455030-11	Patent No. 5455030
1484	106.5	5.9	248	US-08-400-115-4	Sequence 4, Appl
1485	106	5.9	244	US-08-392-338A-13	Sequence 13, Appl
1486	106	5.9	244	US-09-166-750-13	Sequence 13, Appl
1487	106	5.9	244	US-09-166-093-13	Sequence 13, Appl
1488	106	5.9	244	US-09-172-019-13	Sequence 13, Appl
1489	106	5.9	244	US-09-166-094-13	Sequence 13, Appl
1490	106	5.9	244	US-09-443-213-13	Sequence 13, Appl
1491	105.5	5.8	231	US-08-681-432-1	Sequence 1, Appl
1492	105.5	5.8	337	US-08-442-043A-18	Sequence 18, Appl
1493	105.5	5.8	337	US-09-560-639-6	Sequence 6, Appl
1494	105.5	5.8	337	US-08-441-892A-18	Sequence 18, Appl
1495	105.5	5.8	342	US-09-032-337-8	Sequence 41, Appl
1496	105	5.8	63	US-09-397-2430-8	Sequence 8, Appl
1497	105	5.8	63	US-09-397-2430-10	Sequence 10, Appl
1498	105	5.8	269	US-09-949-016-6121	Sequence 6121, Ap
1499	105	5.8	276	US-09-949-016-7261	Sequence 7261, Ap
1500	105	5.8	512	US-08-399-689A-7	Sequence 7, Appl

ALIGNMENTS

US-09-700-397-3
; Sequence 3, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent version 3.0
; SEQ ID NO 3
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Clone OC001 derived from human brain
US-09-700-397-3

Query Match 100.0%; Score 1806; DB 4; Length 344;
Best Local Similarity 100.0%; Pred. No. 3,4e-172;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTIQPKKNSISWAIIFGLALCLFQGVPRSGDATPPKAMDNTVQGSATLRTCTID 60
DB 1 MKTIQPKKNSISWAIIFGLALCLFQGVPRSGDATPPKAMDNTVQGSATLRTCTID 60
QY 61 NRVTVAVMLNSTIIVAGNDKMKCLDPRVVLSNTQTOYSIEIONDVYDEGPYCSVQTD 120
DB 61 NRVTVAVMLNSTIIVAGNDKMKCLDPRVVLSNTQTOYSIEIONDVYDEGPYCSVQTD 120
QY 121 NHPTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTIATSRPEPTVWRIHISPRAGFV 180
DB 121 NHPTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTIATSRPEPTVWRIHISPRAGFV 180
QY 181 SEDYLEIQGITREOSGDYECASNDVAPVVRVRYKVTNTVPYISEAKGTGVPVQKGT 240
DB 181 SEDYLEIQGITREOSGDYECASNDVAPVVRVRYKVTNTVPYISEAKGTGVPVQKGT 240
QY 241 LOCASAVPSAEFQWYKDKRLIEGKGVKVENRPFSLKLPFNVSEHDYGNITCVASNK 300
DB 241 LOCASAVPSAEFQWYKDKRLIEGKGVKVENRPFSLKLPFNVSEHDYGNITCVASNK 300
QY 301 LGHTNASIMLFGPGAVSEVSNCTSRAGCWLPLPLVLHLLKLF 344
DB 301 LGHTNASIMLFGPGAVSEVSNCTSRAGCWLPLPLVLHLLKLF 344

RESULT 2
US-09-700-397-4
; Sequence 4, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent version 3.0
; SEQ ID NO 4
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-700-397-4
Query Match 90.9%; Score 1642; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 7.6e-156;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 RSGDATPPKAMDNTVQGSATLRTCTIDNRVTVAVMLNSTIIVAGNDKMKCLDPRVVLS 91
DB 1 RSGDATPPKAMDNTVQGSATLRTCTIDNRVTVAVMLNSTIIVAGNDKMKCLDPRVVLS 91
QY 92 SNTQTOYSIEIONDVYDEGPYCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINCN 151
DB 61 SNTQTOYSIEIONDVYDEGPYCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINCN 120
QY 152 NISLTCTIATSRPEPTVWRIHISPRAGFVSEDEYLEIQGITREOSGDYECASNDVAPV 211
DB 121 NISLTCTIATSRPEPTVWRIHISPRAGFVSEDEYLEIQGITREOSGDYECASNDVAPV 180
QY 212 VRRVKTNTVPYISEAKGTGVPVQKGTLOCASAVPSAEFQWYKDKRLIEGKGVK 271
DB 181 VRRVKTNTVPYISEAKGTGVPVQKGTLOCASAVPSAEFQWYKDKRLIEGKGVK 240
QY 272 ENRPFLSKLPFNVSEHDYGNITCVASNKLGHTNASIMLFGPGAVSEVSNCTSRAGC 331
DB 241 ENRPFLSKLPFNVSEHDYGNITCVASNKLGHTNASIMLFGPGAVSEVSNCTSRAGC 300
QY 332 LLPVLVHLLKLF 344
DB 301 LLPVLVHLLKLF 313

RESULT 3
US-09-976-594-404
; Sequence 404, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 404
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1640555CD1
US-09-976-594-404

Query Match 51.6%; Score 931.5; DB 4; Length 338;
Best Local Similarity 55.4%; Pred. No. 1.2e-84;
Matches 180; Conservative 60; Mismatches 80; Indels 5; Gaps 4;

QY 20 LALCLF-QGVPRSGDATPPKAMDNTVQGSATLRTCTIDNRVTVAVMLNSTIIVAG 78
DB 17 LRLCLLPYGLPVASVD--FNRGDNITVRQGDYAIRCVLEDKNSKAVAMNRSGLIFAG 74
QY 79 NDKKCLDPRVVLSNTQTOYSIEIONDVYDEGPYCSVQTDNHPKTSRVHLIVQVSPKI 138
DB 75 HDKMSLDPRVLEKRRHSLEYSRLIQKVDYDEGSYTSVQTDHPKTSQVTLIVQVPEKI 134
QY 139 VEISSDISINEGNNISLTCTIATSRPEPTVWRIHISPRAGFVSEDEYLEIQGITREOSGD 198
DB 135 SNISSDVTAVNEGSAVTLVCANGRPEVITTRHLITPGRREGSEBYLEILGIRREGSK 194
QY 199 YECASNDVAPVVRVRYKVTNTVPYISEAKGTGVPVQKGTLOCASAVPSAEFQWYKD 258
DB 199 YECASNDVAPVVRVRYKVTNTVPYISEAKGTGVPVQKGTLOCASAVPSAEFQWYKD 258

Db 195 YECCAANEVSADVKQVTVNYPPTITBSKSNBATTGROASIKCEASAVPADPFEWYRD 254
Qy 259 DKRLIEGKKGVKVENRPFSLKLIFFNVSEHDYGYTCVANSKLGHTNASIMLFGPGAVSE 318
Db 255 DTR-INSANGLERIKSTGQSSLTVTNTBEHYGNITCVAAKNGVTNASLVLPFGSVRG 313
Qy 319 VNSGTSRRACGCVMLPLVLVHLHLK 343
Db 314 I-NGSISIAVPLWMLAASLFLCLSK 337

RESULT 4
US-08-414-657D-42
; Sequence 42, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-414-657D-42

Query Match 51.3%; Score 926.5; DB 2; Length 338;
Best Local Similarity 55.1%; Pred. No. 3.6e-84;
Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;

Qy 20 LAAALCLF-QGVPRSGDATFPKAMDNTVROGSATLRCTIDNRVTRVAMLRSTIIYAG 78
Db 17 LRLCLPLPTGLPVRSDV--FNRGTDNITVROGDTALIRCVVEDGNSKVAMLRSGIIFAG 74
Qy 79 NDKKCLDPRVLLSNTOGYSEIQWVDVYDEGPTCSVGTDNHFKTSRVHLIVQVSPKI 138
Db 75 HDKMSLDPRVLEKRAHLEYSIRIQKVDVYDEGSYTCSVGTGHEPKTSQVYLLIVQVSPKI 134
Qy 139 VEISSDSISGNNISITLTATGRPEPTVMRHTSPKAVGVSEDEYLEIOGIRBOSGD 198
Db 135 SNISSDVTNBSGNTLVCCANGRPEPTVTRHLPLUGREPEGEELYLEIGITRBOSGK 194

Qy 199 YECASNDVAAPVRRVKTVNYPPIYSEAKGTGVVGOKGTLQCEASAVPSAEFOWYKD 258
Db 195 YECCAANEVSADVKQVTVNYPPTITBSKSNBATTGROASIKCEASAVPADPFEWYRD 254
Qy 259 DKRLIEGKKGVKVENRPFSLKLIFFNVSEHDYGYTCVANSKLGHTNASIMLFGPGAVSE 318
Db 255 DTR-INSANGLERIKSTGQSSLTVTNTBEHYGNITCVAAKNGVTNASLVLPFGSVRG 313
Qy 319 VNSGTSRRACGCVMLPLVLVHLHLK 343
Db 314 I-NGSISIAVPLWMLAASLFLCLSK 337

RESULT 5
US-08-414-657D-43
; Sequence 43, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-414-657D-43

Query Match 51.3%; Score 926.5; DB 2; Length 338;
Best Local Similarity 55.1%; Pred. No. 3.6e-84;
Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;

Qy 20 LAAALCLF-QGVPRSGDATFPKAMDNTVROGSATLRCTIDNRVTRVAMLRSTIIYAG 78
Db 17 LRLCLPLPTGLPVRSDV--FNRGTDNITVROGDTALIRCVVEDGNSKVAMLRSGIIFAG 74
Qy 79 NDKKCLDPRVLLSNTOGYSEIQWVDVYDEGPTCSVGTDNHFKTSRVHLIVQVSPKI 138
Db 75 HDKMSLDPRVLEKRAHLEYSIRIQKVDVYDEGSYTCSVGTGHEPKTSQVYLLIVQVSPKI 134

MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-135-080-2

Query Match 51.1%; Score 923.5; DB 4; Length 325;
Best Local Similarity 55.3%; Pred. No. 6,8e-84;
Matches 177; Conservative 60; Mismatches 78; Indels 5; Gaps 4;

QY LAALCLF-QGVPRVSGDTPKAMDNTVRQGSATLRCTIDNVTAVAMINRSTILYAG 78
DB LRLCLPTGLPVSVD--FNRGTDNITVRQGDALRLCVLEDKSKVAMINRSGIIPAG 67
QY 79 NDKWCLDPRVLLSNTQVSIETQNDVYDEGPTSCVQTDNPKTSRVHLIVQVSPKI 138
DB 68 HDKMSLDPRVLELRHSLRISLRIOKVDVDEGSYTSVQTOHPEKTSQVLLIVQVPEKI 127
QY 139 VEISDSINEGNNISLTCLATGRPEPTVTRHISPRKAVGVSEDEYLEIQITREOSGD 198
DB 128 SNISSDVTVNEGSVTLVCMANGRPVITWRHLPTGRFEGEGBEYLEILGITREOSGK 187
QY 199 YECASNDVAPVVRVRYVTNYPPIYSEAKGTGPVQOKGTLQCEASAVPSAEFQWYKD 258
DB 188 YECANAEVSADVKQVKVTNYPPTITSEKSNBATTRQASLCEASAVPAPDFEWRD 247
QY 259 DKRLIEGKGVKVENRPFSLTIFPNVSEHDYGYTCVASNKLGHNTASIMLFGPGAVSE 318
DB 248 DTR-INSANGLEISTEGQSSLTVTWTEHYGYTCVAANKLGVNASLVLFRPGSVRG 306
QY 319 VSNGTSRRAGCWMLLPLVL 338
DB 307 I-NGSISLAVPLWMLAASLL 325

RESULT 10

US-08-414-657D-60

Sequence 60, Application US/08414657D

Patent No. 5861283

GENERAL INFORMATION:

APPLICANT: Levitt, Pat

APPLICANT: Pimenta, Aurea

APPLICANT: Fischer, Itzhak

APPLICANT: Zhukareva, Victoria

TITLE OF INVENTION: Lambic System-Associated Membrane

TITLE OF INVENTION: Protein and DNA

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Dechert Price & Rhoads

STREET: 997 Lenox Drive, Building 3, Suite 210

CITY: Lawrenceville

STATE: NJ

COUNTRY: USA

ZIP: 08543

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/414,657D

FILING DATE: 31-MAR-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Bloom, Allen

REGISTRATION NUMBER: 29,135

REFERENCE/DOCKET NUMBER: 317743-102

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-520-3214

TELEFAX: 609-520-3259

TELEX:

INFORMATION FOR SEQ ID NO: 60:

SEQUENCE CHARACTERISTICS:
LENGTH: 338 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-414-657D-60

Query Match 51.1%; Score 923.5; DB 2; Length 338;
Best Local Similarity 55.1%; Pred. No. 7,3e-84;
Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRVSGDTPKAMDNTVRQGSATLRCTIDNVTAVAMINRSTILYAG 78
DB 17 LRLCLPTGLPVSVD--FNRGTDNITVRQGDALRLCVLEDKSKVAMINRSGIIPAG 74
QY 79 NDKWCLDPRVLLSNTQVSIETQNDVYDEGPTSCVQTDNPKTSRVHLIVQVSPKI 138
DB 75 HDKMSLDPRVLELRHSLRISLRIOKVDVDEGSYTSVQTOHPEKTSQVLLIVQVPEKI 134
QY 139 VEISDSINEGNNISLTCLATGRPEPTVTRHISPRKAVGVSEDEYLEIQITREOSGD 198
DB 135 SNISSDVTVNEGSVTLVCMANGRPVITWRHLPTGRFEGEGBEYLEILGITREOSGK 194
QY 199 YECASNDVAPVVRVRYVTNYPPIYSEAKGTGPVQOKGTLQCEASAVPSAEFQWYKD 258
DB 195 YECANAEVSADVKQVKVTNYPPTITSEKSNBATTRQASLCEASAVPAPDFEWRD 254
QY 259 DKRLIEGKGVKVENRPFSLTIFPNVSEHDYGYTCVASNKLGHNTASIMLFGPGAVSE 318
DB 255 DTR-INSANGLEISTEGQSSLTVTWTEHYGYTCVAANKLGVNASLVLFRPGSVRG 313
QY 319 VSNGTSRRAGCWMLLPLVLHL 343
DB 314 I-NGSISLAVPLWMLAASLCLSLK 337

RESULT 11

US-09-135-080-8

Sequence 8, Application US/09135080

Patent No. 6423827

GENERAL INFORMATION:

APPLICANT: Levitt, Pat R.

APPLICANT: Pimenta, Aurea

APPLICANT: Fischer, Itzhak

APPLICANT: Zhukareva, Victoria

TITLE OF INVENTION: Lambic System-Associated Membrane

TITLE OF INVENTION: Protein and DNA

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Dechert Price & Rhoads

STREET: 997 Lenox Drive, Building 3, Suite 210

CITY: Lawrenceville

STATE: NJ

COUNTRY: USA

ZIP: 08543

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/135,080

FILING DATE: 17-AUG-1998

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/414,657

FILING DATE: 31-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bloom, Allen

REGISTRATION NUMBER: 29,135

REFERENCE/DOCKET NUMBER: 317743-102A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-620-3214

TELEFAX: 609-620-3259
 TELEPHONE: 609-520-3214
 TELEFAX: 609-520-3259
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 338 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-135-080-8

Query Match 51.1%; Score 923.5; DB 4; Length 338;
 Best Local Similarity 55.1%; Pred. No. 7.3e-84;
 Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDAPPKANDVTYVQGSATLRCITDNRVTWAMLNRSITLYAG 78
 Db LRLCLPLTGLPVRSD--FNRGTDNITVQGDITLRCVLEDRKNSKVAMLNRSGITIFAG 74
 QY 79 NDKWCLDPRVVLSTNTQVYSIEIQNDVYDEGPTCSVQTDNHPKTSRVLIVQVSPKI 138
 Db HDKMSLDPRVLEKRSLSLEYSIRIQKVDYDEGSYTSVQTHHPKTSQVYLLIVQVSPKI 134
 QY 139 VEISDSISINEGNISITCIATGRPEPTVTRHISPKAVGFVSEDEYLETIGITREOSGD 198
 Db 135 SNISSDVTVEGSAVTLVCANGRPEPTVTRHILTPGRFEFESEETLEITIGITREOSGD 194
 QY 199 YECASNDVAPVVRKVTVPYPISEAKGTGVPVQKGLQCEASAVPAPAFQWYKD 258
 Db 195 YECASNDVAPVVRKVTVPYPISEAKGTGVPVQKGLQCEASAVPAPAFQWYKD 254
 QY 259 DKRLIEGKGVKVRNPFSLKLIFFNVSEHDYGYTCVANSKLGHTNASIMLPFGAVSE 318
 Db 255 DTR-INSANGLERKSTEGQSLVTVTWTEHYGNYTCVANKLGVTNASIMLPFGAVSVRG 313
 QY 319 VNSGTSRAGCVMPLPLVHLHLK 343
 Db 314 I-NGSISLAVPLMLASLCLSK 337

RESULT 12
 US-08-414-657D-46
 ; Sequence 46, Application US/08414657D
 ; Patent No. 5861283
 ; GENERAL INFORMATION:
 ; APPLICANT: Levitt, Pat
 ; APPLICANT: Pimenta, Aurea
 ; APPLICANT: Fischer, Itzhak
 ; APPLICANT: Zhukareva, Victoria
 ; TITLE OF INVENTION: Limbic System-Associated Membrane
 ; TITLE OF INVENTION: Protein and DNA
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dechert Price & Rhoads
 ; STREET: 997 Lenox Drive, Building 3, Suite 210
 ; CITY: Lawrenceville
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08543
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/414,657D
 ; FILING DATE: 31-MAR-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bloom, Allen
 ; REGISTRATION NUMBER: 29,135

REFERENCE/DOCKET NUMBER: 317743-102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-520-3214
 TELEFAX: 609-520-3259
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 308 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-414-657D-46

Query Match 50.3%; Score 908; DB 2; Length 308;
 Best Local Similarity 56.3%; Pred. No. 2.2e-82;
 Matches 170; Conservative 58; Mismatches 70; Indels 4; Gaps 3;

QY 20 LAALCLF-QGVPRSGDAPPKANDVTYVQGSATLRCITDNRVTWAMLNRSITLYAG 78
 Db 10 LRLCLPLTGLPVRSD--FNRGTDNITVQGDITLRCVLEDRKNSKVAMLNRSGITIFAG 67
 QY 79 NDKWCLDPRVVLSTNTQVYSIEIQNDVYDEGPTCSVQTDNHPKTSRVLIVQVSPKI 138
 Db 68 HDKMSLDPRVLEKRSLSLEYSIRIQKVDYDEGSYTSVQTHHPKTSQVYLLIVQVSPKI 127
 QY 139 VEISDSISINEGNISITCIATGRPEPTVTRHISPKAVGFVSEDEYLETIGITREOSGD 198
 Db 128 SNISSDVTVEGSAVTLVCANGRPEPTVTRHILTPGRFEFESEETLEITIGITREOSGD 187
 QY 199 YECASNDVAPVVRKVTVPYPISEAKGTGVPVQKGLQCEASAVPAPAFQWYKD 258
 Db 188 YECASNDVAPVVRKVTVPYPISEAKGTGVPVQKGLQCEASAVPAPAFQWYKD 247
 QY 259 DKRLIEGKGVKVRNPFSLKLIFFNVSEHDYGYTCVANSKLGHTNASIMLPFGAVSE 318
 Db 248 DTR-INSANGLERKSTEGQSLVTVTWTEHYGNYTCVANKLGVTNASIMLPFGAVSVRG 306
 QY 319 VS 320
 Db 307 IN 308

RESULT 13
 US-08-414-657D-47
 ; Sequence 47, Application US/08414657D
 ; Patent No. 5861283
 ; GENERAL INFORMATION:
 ; APPLICANT: Levitt, Pat
 ; APPLICANT: Pimenta, Aurea
 ; APPLICANT: Fischer, Itzhak
 ; APPLICANT: Zhukareva, Victoria
 ; TITLE OF INVENTION: Limbic System-Associated Membrane
 ; TITLE OF INVENTION: Protein and DNA
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dechert Price & Rhoads
 ; STREET: 997 Lenox Drive, Building 3, Suite 210
 ; CITY: Lawrenceville
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08543
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/414,657D
 ; FILING DATE: 31-MAR-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:

```

/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bloom, Allen
/ REGISTRATION NUMBER: 29,135
/ REFERENCE/DOCKET NUMBER: 317743-102
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 609-520-3214
/ TELEFAX: 609-520-3259
/
/ INFORMATION FOR SEQ ID NO: 47:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 315 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-414-657D-47

Query Match          50.2%; Score 907; DB 2; Length 315;
Best Local Similarity 56.3%; Pred. No. 2,9e-82;
Matches 170; Conservative 58; Mismatches 70; Indels 4; Gaps 3;

QY 20 LAALCLFQGVVRSQDTPPKAMDNVTVRQGESATLCTIDNRTVAMLNKSTILVAG 78
DB 17 LRLCLLPTGLPVSVSD--FNRGTDNITVRQGDTRILRCVVEDKNSKVMALNRSGLIPAG 74
QY 79 NDKMCLDPRVLLSNTQTVSIEIQNDVYDEGPTCSVQTDNHPKTSRVHLIVQVSEPKI 138
DB 75 HDKMSLDPRVELKRMHLESLRIQKVVDYDEGYSVQVQHEPKTSQVYLLIVQVPEKI 134
QY 139 VEISGDSISNGNNISLTCTIATGRPEPTVTRHISPKAVGVSEDEYELIGITRQSGD 198
DB 135 SNISSDVTVNGSVNTLVCMANGRPEPVITWRHLPLDREBEGEBEYELIIGITRQSGK 194
QY 199 YEGSANDVAVVRVRYVTNVPYVISEAKGTGVPVGKTLQCEASAVPSAFQWPKD 258
DB 195 YECRAAEVSSADVQVAVTNVPTPTTESKSNBATGTRQASLKCSAVPADPFWYRDRD 254
QY 259 DKRLIEGKGVKVENRPFSLIFPNVSEHDYGVTCVANSKLGHTNASIMLFGPGAVSE 318
DB 255 DTR-INSANGLEISTEGSSSLVTNVTBEHYGVTCVANKLGVTNASLVLPFGSVRG 313
QY 319 VS 320
DB 314 IN 315

RESULT 14
US-08-414-657D-45
/ Sequence 45, Application US/08414657D
/ Patent No. 5861283
/ GENERAL INFORMATION:
/ APPLICANT: Levitt, Pat
/ APPLICANT: Pimenta, Aurea
/ APPLICANT: Fischer, Itzhak
/ APPLICANT: Zhukareva, Victoria
/ TITLE OF INVENTION: Lambic System-Associated Membrane
/ TITLE OF INVENTION: Protein and DNA
/ NUMBER OF SEQUENCES: 60
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dechert Price & Rhoads
/ STREET: 997 Lenox Drive, Building 3, Suite 210
/ CITY: Lawrenceville
/ STATE: NJ
/ COUNTRY: USA
/ ZIP: 08543
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ FILING DATE: 31-MAR-1995
/ CLASSIFICATION: 435

```

```

/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bloom, Allen
/ REGISTRATION NUMBER: 29,135
/ REFERENCE/DOCKET NUMBER: 317743-102
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 609-520-3214
/ TELEFAX: 609-520-3259
/
/ INFORMATION FOR SEQ ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 310 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-414-657D-45

Query Match          50.1%; Score 905; DB 2; Length 310;
Best Local Similarity 55.3%; Pred. No. 4,5e-82;
Matches 173; Conservative 59; Mismatches 77; Indels 4; Gaps 3;

QY 31 VRSGDATPPKAMDNVTVRQGESATLCTIDNRTVAMLNKSTILVAGNDKMLDPRVVL 90
DB 1 VRSDV--FNRGTDNITVRQGDTRILRCVVEDKNSKVMALNRSGLIPAGHDKMSLDPRVEL 58
QY 91 LNSTQTVSIEIQNDVYDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEG 150
DB 59 EKRAHLEYSRLIQKVVDYDEGYSVQVQHEPKTSQVYLLIVQVPPKISNISDVTVNEG 118
QY 151 NNISLTCTIATGRPEPTVTRHISPKAVGVSEDEYELIGITRQSGDYECASANDVAAP 210
DB 119 SNVTLVCMANGRPEPVITWRHLPLDREBEGEBEYELIIGITRQSGKYECKANRVSAA 178
QY 211 VRRRVKTVNVPYVISEAKGTGVPVGKTLQCEASAVPSAFQWYDKRLIEGKGVK 270
DB 179 DVKQVKTVNVPPTPTTESKSNBATGTRQASLKCSAVPADPFWYRDRDTR-INSANGLE 237
QY 271 VERNRPFSLKLIFFNVSEHDYGVTCVANSKLGHTNASIMLFGPGAVSEVSGTRRACV 330
DB 238 IKSTEGSSSLVTNVTBEHYGVTCVANKLGVTNASLVLPFGSVRGI-NGSISLAVPL 296
QY 331 WLPLVLYLHLK 343
DB 297 WLAAALFCLLSK 309

RESULT 15
US-08-414-657D-44
/ Sequence 44, Application US/08414657D
/ Patent No. 5861283
/ GENERAL INFORMATION:
/ APPLICANT: Levitt, Pat
/ APPLICANT: Pimenta, Aurea
/ APPLICANT: Fischer, Itzhak
/ APPLICANT: Zhukareva, Victoria
/ TITLE OF INVENTION: Lambic System-Associated Membrane
/ TITLE OF INVENTION: Protein and DNA
/ NUMBER OF SEQUENCES: 60
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dechert Price & Rhoads
/ STREET: 997 Lenox Drive, Building 3, Suite 210
/ CITY: Lawrenceville
/ STATE: NJ
/ COUNTRY: USA
/ ZIP: 08543
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/414,657D
 FILING DATE: 31-MAR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Bloom, Allen
 REGISTRATION NUMBER: 29,135
 REFERENCE/DOCKET NUMBER: 317743-102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-520-3214
 TELEFAX: 609-520-3259
 TELLEX:
 INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 304 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-414-657D-44

Query Match	49.9%;	Score 902;	DB 2;	Length 304;
Best Local Similarity	55.5%;	Pred. No. 8.7e-82;		
Matches 171;	Conservative 59;	Mismatches 74;	Indels 4;	Gaps 3;

Qy	31	VRSGDGTTPKAMDNVTVRGSGSATRTCTIDNRVTEVAALNSTLLVYGNKWCICLDPVVL	90
Db	1	VRSDVD--FRRGDNIITVRGDGTALIRCVLEIDKNSKVMALNNSGIIIPAGHDKMSLDPVEL	58
Qy	91	LSNTQOQYSLEIONDVDEBPGYTSVQTDNHFKTSRPHLLVOVSPKIVLEISDLSINEG	150
Db	59	EKRHSLEYLRIOKDVVDDEGYSVTQOHEPKISQVYLLIVQVPEKISNISDVTNEG	118
Qy	151	NNISLTCIATGRPEPTVTRHRSIPKAVGVSEDEYLTICQITRQSGDGYECCASNDVAAP	210
Db	119	SNVTLICMANGRPEVITWRHLTPGRREBGEERLELTIGITRQSGKYECKAMNEVSSA	178
Qy	211	VVRVRYTVNNPPYISAEAKGTVPVQKGTLOCEASAVPSAEFQMYKODKRLIEGKGKGV	270
Db	179	DVQVQVTVNNPPYITPESKSNBATGRQASLKCEASAVPADPFMYRDRDR--INSANGLE	237
Qy	271	VENRPPLSKLIFPNVSEHDYGNVTCVANSKLGHTNASIMLPGAPAVSEVNSGTSRRAGCV	330
Db	238	IKSTEGQSSILTVNNTVEHYGNVTCVANKKGVNTNASTLVLRPDSVNGI--NGSISLAVPL	296
Qy	331	WLPLPLVL	338
Db	297	WLLASL	304

Search completed: June 3, 2005, 14:38:08
Job time : 34 secs

GenCore version 5.1.6
OM protein - protein search, using sw model
Run on: June 3, 2005, 14:09:27 ; Search time 73 Seconds
(without alignments)
1822.542 Million cell updates/sec

Title: US-09-978-544A-523
Perfect score: 1806
Sequence: 1 MKTIQPMKMSISWAIPTGL.....RRACQWLLPLVLLHLKLF 344
Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5
2105692
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
A_Geneseq_16Dec04:*

- 1: geneeqp1980s:*
- 2: geneeqp1990s:*
- 3: geneeqp2000s:*
- 4: geneeqp2001s:*
- 5: geneeqp2002s:*
- 6: geneeqp2003as:*
- 7: geneeqp2003bs:*
- 8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match Length	DB ID	Description
RESULT 1				
ID	AAV57601	standard; protein; 344 AA.		
DE	Human protein SEQ ID NO:1.			
PN	WO958668-A1.			
PD	18-NOV-1999.			
PA	(ONOV) ONO PHARM CO LTD.			
Query Match	100.0%;	Score 1806; DB 3;	Length 344;	
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 2				
ID	AA44329	standard; protein; 344 AA.		
DE	Human PRO337 protein sequence SEQ ID NO:523.			
PN	WO200053756-A2.			
PD	14-SEP-2000.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806; DB 3;	Length 344;	
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 3				
ID	AA31204	standard; protein; 344 AA.		
DE	Amino acid sequence of human polypeptide PRO337.			
PN	WO200077037-A2.			
PD	21-DEC-2000.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806; DB 4;	Length 344;	
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 4				
ID	AAU12359	standard; protein; 344 AA.		
DE	Human PRO337 polypeptide sequence.			
PN	WO200140466-A2.			
PD	07-JUN-2001.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806; DB 4;	Length 344;	
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 5				
ID	AA083654	standard; protein; 344 AA.		
DE	Human PRO protein, Seq ID NO 126.			
PN	WO200208288-A2.			
PD	31-JAN-2002.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806; DB 5;	Length 344;	
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 6				
ID	ABB84844	standard; protein; 344 AA.		

DE	Human PRO337 protein sequence SEQ ID NO:56.			
PN	WO200200690-A2.			
PD	03-JAN-2002.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806; DB 5;	Length 344;	
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 7				
ID	AB95450	standard; protein; 344 AA.		
DE	Human angiogenesis related protein PRO337 SEQ ID NO: 56.			
PN	WO200208284-A2.			
PD	31-JAN-2002.			
PA	(GETH) GENENTECH INC.			
PA	(BAKE) BAKER K P.			
PA	(FERR) FERRARA N.			
PA	(GERB) GERBER H.			
PA	(GERR) GERRITSEN M E.			
PA	(GODD) GODDARD A.			
PA	(GODO) GODONSKI P J.			
PA	(GURN) GURNEY A L.			
PA	(HILL) HILLAN K J.			
PA	(MARS) MARSTERS S A.			
PA	(PANJ) PAN J.			
PA	(PRON) PRONI N F.			
PA	(STEP) STEPHAN J F.			
PA	(WATA) WATANABE C K.			
PA	(WILL) WILLIAMS P M.			
PA	(WOOD) WOOD W I.			
Query Match	100.0%;	Score 1806; DB 5;	Length 344;	
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 8				
ID	AB017803	standard; protein; 344 AA.		
DE	Novel human secreted and transmembrane protein PRO337.			
PN	US2003032156-A1.			
PD	13-FEB-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806; DB 6;	Length 344;	
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 9				
ID	ABU80801	standard; protein; 344 AA.		
DE	Human PRO polypeptide #63.			
PN	US2003036635-A1.			
PD	20-FEB-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806; DB 6;	Length 344;	
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 10				
ID	AB025175	standard; protein; 344 AA.		
DE	Novel human secreted and transmembrane protein PRO337.			
PN	US2003040014-A1.			
PD	27-FEB-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806; DB 6;	Length 344;	
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 11				
ID	AB025275	standard; protein; 344 AA.		
DE	Novel human secreted and transmembrane protein PRO337.			
PN	US2003050239-A1.			
PD	13-MAR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806; DB 6;	Length 344;	
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 12				
ID	AB033767	standard; protein; 344 AA.		
DE	Novel human secreted and transmembrane protein PRO337.			
PN	US2003045687-A1.			
PD	06-MAR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806; DB 6;	Length 344;	
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 13				
ID	ABU81057	standard; protein; 344 AA.		
DE	Human PRO polypeptide #188.			
PN	US2003040311-A1.			

PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 14
ID ABU7281 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 15
ID ABU6757 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 16
ID ABU67293 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 17
ID ABU84961 standard; protein; 344 AA.
DE Human secreted and transmembrane PRO polypeptide #37.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 18
ID ABUS938 standard; protein; 344 AA.
DE Novel secreted and transmembrane protein PRO337.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 19
ID ABU61159 standard; protein; 344 AA.
DE Human PRO337 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 20
ID ABO25028 standard; protein; 344 AA.
DE Human secreted/transmembrane protein (PRO) #188.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 21
ID ABU72061 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 22
ID ABU67162 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003032062-A1.
PD 13-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 23
ID ABU80428 standard; protein; 344 AA.
DE Human secreted/transmembrane protein PRO337.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 24
ID ABU82110 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 25
ID ABU6703 standard; protein; 344 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 376.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 26
ID ABU79804 standard; protein; 344 AA.
DE Human secreted/transmembrane protein PRO337.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 27
ID ADA45895 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003023232-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 28
ID ADA76326 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 29
ID ABJ72290 standard; protein; 344 AA.
DE Human PRO337 protein.
PN US2003050446-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 30
ID ADA18976 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 31
ID ADA61599 standard; protein; 344 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 32
ID ADB19384 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 33
ID ADB27925 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 34
ID ADA86404 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 35
ID ADB15968 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 36
ID ADA47754 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 37
ID ADA67549 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 38
ID ADB30556 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 39
ID ADA8552 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 40
ID ADA97064 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;

Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 41
ID ADA79368 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 42
ID ADA87507 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 43
ID ADB16709 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 44
ID ADA91801 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 45
ID ADB14864 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 46
ID ADA25062 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 47
ID ADA47276 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO337.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 48
ID ADB18825 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 49
ID ADA94040 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;

RESULT 50
ID ADB19936 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 51
ID ADB13248 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 52
ID ABO4336 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 53
ID ABO19730 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 54
ID ADA1723 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO337.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 55
ID ADA74502 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 56
ID ADB24735 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 57
ID ADA82259 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 58
ID ADA75222 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 59
ID ADB31108 standard; protein; 344 AA.

ID ADA85300 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 60
ID ADA84748 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 61
ID ADB30004 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 62
ID ADA80532 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 63
ID ADA75774 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 64
ID ADA46999 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 65
ID ADB25295 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 66
ID ADA93471 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 67
ID ADB26821 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 68
ID ADB31108 standard; protein; 344 AA.

DE Human PRO polypeptide #188.
 PN US2003096386-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 69
 ID ABJ72418 standard; protein; 344 AA.
 DE Human PRO337 protein.
 PN US2003027988-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 70
 ID ADA61036 standard; protein; 344 AA.
 DE Homo sapiens.
 PN US2003049817-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 71
 ID ADB24183 standard; protein; 344 AA.
 DE Human PRO polypeptide SEQ ID NO 376.
 PN US2003077714-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 72
 ID ADA96512 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003082690-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 73
 ID ADA81084 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003082702-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 74
 ID ADA95960 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003082759-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 75
 ID ADB26269 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003082760-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 76
 ID ADB21754 standard; protein; 344 AA.
 DE Novel human secreted and transmembrane protein PRO337.
 PN US2003082765-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 77
 ID ABO34313 standard; protein; 344 AA.
 DE Human secreted/transmembrane polypeptide PRO 337.
 PN US2003044934-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 78
 ID ABO19621 standard; protein; 344 AA.
 DE Novel human secreted and transmembrane polypeptide #89.
 PN US2003049633-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 6; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 79
 ID ADA7533 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003068797-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 7; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 80
 ID ADB18273 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003077710-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 7; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 81
 ID ADA86956 standard; protein; 344 AA.
 DE Novel human secreted and transmembrane protein PRO337.
 PN US2003082709-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 7; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 82
 ID ADA88059 standard; protein; 344 AA.
 DE Novel human secreted and transmembrane protein PRO337.
 PN US2003082700-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 7; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 83
 ID ADA46447 standard; protein; 344 AA.
 DE Novel human secreted and transmembrane protein PRO337.
 PN US2003054516-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 7; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 84
 ID ADB28477 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003082699-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 7; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 85
 ID ADB29029 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003082706-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 7; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 86
 ID ADA76981 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003059909-A1.
 PD 27-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 87
ID ADA8611 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 88
ID ADA97616 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 89
ID ADB27373 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 90
ID ADB23306 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 91
ID ABO19862 standard; protein; 344 AA.
DE Human secreted/transmembrane protein PRO337.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 92
ID AB72120 standard; protein; 344 AA.
DE Human membrane bound receptor/protein PRO337 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 93
ID ADA66997 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 94
ID ADB22858 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 95
ID ADB23631 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;

RESULT 96
ID ADA93353 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 97
ID ADB15416 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 98
ID ADB83616 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 99
ID ADB80722 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 100
ID ADB73263 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 101
ID ADB38668 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 102
ID ADB78345 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 103
ID ADB38116 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 104
ID ADB66588 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 105

ID ADB84993 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 106
ID ADB89668 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 107
ID ADB90400 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 108
ID ADB39501 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 109
ID ADB78099 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 110
ID ADB74029 standard; protein; 344 AA.
DE Human PRO polypeptide #89.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 111
ID ADB87165 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 112
ID ADB84747 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 113
ID ADB47124 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 114
ID ADB83862 standard; protein; 344 AA.

DE Novel human secreted and transmembrane protein PRO337.
PN US200306397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 115
ID ADB86731 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 116
ID ADB73017 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 117
ID ADB76745 standard; protein; 344 AA.
DE Human PRO polypeptide #89.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 118
ID ADB77336 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 119
ID ADB34493 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 120
ID ADB35597 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 121
ID ADB33941 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 122
ID ADB35045 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 123
ID ADB36149 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.

PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 124
ID ADB46544 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 125
ID ADC44171 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 126
ID ADC61931 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 127
ID ADC63895 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 128
ID ADC66995 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 129
ID ADC69119 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 130
ID ADC63179 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003068646-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 131
ID ADC68244 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 132
ID ADC41564 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003072745-A1.

PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 133
ID ADC67619 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 134
ID ADC62555 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 135
ID ADC36855 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 136
ID ADC42188 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 137
ID ADC21845 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 138
ID ADC50417 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 139
ID ADC71964 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 140
ID ADC59943 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 141
ID ADC49876 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088064-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 142
ID ADC49075 standard; protein: 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 143
ID ADC49592 standard; protein: 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 144
ID ADC47453 standard; protein: 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 145
ID ADC52950 standard; protein: 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 146
ID ADC57304 standard; protein: 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 147
ID ADC60495 standard; protein: 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 148
ID ADC50970 standard; protein: 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 149
ID ADC65497 standard; protein: 344 AA.
DE Human PRO polypeptide #188.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 150
ID ADC54595 standard; protein: 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 151
ID ADC5556 standard; protein: 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 152
ID ADC59079 standard; protein: 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 153
ID ADC5957 standard; protein: 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 154
ID ADC58527 standard; protein: 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 155
ID ADC47198 standard; protein: 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 156
ID ADD03201 standard; protein: 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 157
ID ADC90193 standard; protein: 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 158
ID ADC69612 standard; protein: 344 AA.
DE Human PRO polypeptide #188.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 159
ID ADC48501 standard; protein: 344 AA.
DE Human PRO polypeptide #188.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 160
ID ADC54595 standard; protein: 344 AA.
DE Novel human secreted and transmembrane protein Seq ID376.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;

Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 160
ID ADD10030 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 161
ID APC78073 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 162
ID ADD04605 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 163
ID ADD06308 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 164
ID ADC80561 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 165
ID ADD11068 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 166
ID ADD10345 standard; protein; 344 AA.
DE Human secreted/transmembrane PRO polypeptide #28.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 167
ID ADC47949 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 168
ID ADC77827 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;

RESULT 169
ID ADC80009 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 170
ID ADD11305 standard; protein; 344 AA.
DE Human secreted/transmembrane PRO polypeptide #28.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 171
ID ADD09478 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 172
ID ADD50790 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 173
ID ADD41191 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 174
ID ADD52330 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 175
ID ADD51036 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 176
ID ADD53070 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 177
ID ADD53622 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 178

ID ADD37098 standard; protein, 344 AA.
DE Human secreted/cranmembrane PRO polypeptide #28.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 179
ID ADD51778 standard; protein, 344 AA.
DE Human PRO polypeptide #188.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 180
ID ADD02577 standard; protein, 344 AA.
DE Human PRO polypeptide #188.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 181
ID ADD50517 standard; protein, 344 AA.
DE Human PRO polypeptide #63.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 182
ID ADD02011 standard; protein, 344 AA.
DE Human PRO polypeptide #188.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 183
ID ADD54193 standard; protein, 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 184
ID ADD50271 standard; protein, 344 AA.
DE Human PRO polypeptide #63.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 185
ID ADD51282 standard; protein, 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 186
ID ADE49557 standard; protein, 344 AA.
DE Human secreted/cranmembrane protein, PRO337.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 187
ID ADD92510 standard; protein, 344 AA.

DE Human PRO polypeptide #188.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 188
ID ADD91406 standard; protein, 344 AA.
DE Human PRO polypeptide #188.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 189
ID ADE04020 standard; protein, 344 AA.
DE Human PRO polypeptide #188.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 190
ID ADE32317 standard; protein, 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 191
ID ADE22249 standard; protein, 344 AA.
DE Human PRO polypeptide #188.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 192
ID ADD79473 standard; protein, 344 AA.
DE Human PRO polypeptide #188.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 193
ID ADE35611 standard; protein, 344 AA.
DE Human secreted/cranmembrane protein, PRO337.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 194
ID ADE16725 standard; protein, 344 AA.
DE Human secreted/cranmembrane protein, PRO337.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 195
ID ADD73340 standard; protein, 344 AA.
DE Human secreted/cranmembrane protein, PRO337.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 196
ID ADE42009 standard; protein, 344 AA.
DE Human PRO polypeptide #188.

PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 197
ID ADE17826 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 198
ID ADD91958 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 199
ID ADE33421 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 200
ID ADE33973 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 201
ID ADD80025 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 202
ID ADD93062 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 203
ID ADD72698 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 204
ID ADE19482 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 205
ID ADE18930 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199026-A1.

PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 206
ID ADE43126 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 207
ID ADD95915 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 208
ID ADE22801 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 209
ID ADD78919 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 210
ID ADE32869 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 211
ID ADE42561 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 212
ID ADE17349 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 213
ID ADD80577 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 214
ID ADD89605 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199028-A1.
PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 215
ID ADE40869 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 216
ID ADE04688 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 217
ID ADE92817 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 218
ID ADE47363 standard; protein; 344 AA.
DE Human secreted/transmembrane protein; PRO337.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 219
ID ADE21526 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 220
ID ADE23167 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 221
ID ADE97502 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 222
ID ADE80566 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 223
ID ADE53120 standard; protein; 344 AA.
DE Human secreted/transmembrane protein; PRO337.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 224
ID ADE60440 standard; protein; 344 AA.
DE Human secreted/transmembrane protein; PRO337.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 225
ID ADE80014 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 226
ID ADE63785 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO337.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 227
ID ADE55306 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 228
ID ADE55858 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 229
ID ADE161200 standard; protein; 344 AA.
DE Human secreted/transmembrane protein; PRO337.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 230
ID ADE164077 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 231
ID ADE165026 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 232
ID ADE163525 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 233
ID ADE163525 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;

Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 233
ID ADH81939 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 234
ID ADH81387 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 235
ID ADM8256 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 236
ID ADN1595 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 237
ID ADN1584 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 238
ID ADN15403 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 239
ID ADN14851 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 240
ID ADC4829 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 241
ID ADC8113 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;

RESULT 242
ID ADE21000 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 243
ID ADE0584 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 244
ID ADD76561 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 245
ID ADD75073 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 246
ID ADD75819 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 247
ID ADD85051 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 248
ID ADD86877 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 249
ID ADE20754 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 250
ID ADE39051 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 251

ID ADD87925 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003092113-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 252

ID ADD86329 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003203440-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 253

ID ADE05598 standard; protein; 344 AA.
 DE Human PRO polypeptide #63.
 PN US2003100727-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 254

ID ADD73583 standard; protein; 344 AA.
 DE Human PRO polypeptide #63.
 PN US2003100711-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 255

ID ADE75777 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003211571-A1.
 PD 13-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 256

ID ADE48857 standard; protein; 344 AA.
 DE Human secreted/transmembrane protein, PRO337.
 PN US2003104536-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 257

ID ADD78423 standard; protein; 344 AA.
 DE Novel human secreted and transmembrane protein PRO337.
 PN US2003100737-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 258

ID ADE41306 standard; protein; 344 AA.
 DE Human secreted/transmembrane PRO polypeptide #28.
 PN US2003100497-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 259

ID ADE23353 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003092108-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 260

ID ADE21246 standard; protein; 344 AA.

DE Novel human secreted and transmembrane protein PRO337.
 PN US2003100736-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 261

ID ADD77361 standard; protein; 344 AA.
 DE Novel human secreted and transmembrane protein PRO337.
 PN US2003100732-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 262

ID ADE20508 standard; protein; 344 AA.
 DE Novel human secreted and transmembrane protein PRO337.
 PN US2003100733-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 263

ID ADD75573 standard; protein; 344 AA.
 DE Human PRO polypeptide #63.
 PN US2003100064-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 264

ID ADD74089 standard; protein; 344 AA.
 DE Human PRO polypeptide #63.
 PN US2003100708-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 265

ID ADD74335 standard; protein; 344 AA.
 DE Human PRO polypeptide #63.
 PN US2003100709-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 266

ID ADD76065 standard; protein; 344 AA.
 DE Novel human secreted and transmembrane protein PRO337.
 PN US2003100718-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 267

ID ADE85557 standard; protein; 344 AA.
 DE Novel human secreted and transmembrane protein PRO337.
 PN US2003100721-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 268

ID ADE23905 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003092110-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 269

ID ADE24548 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.

PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 270
ID ADD87373 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 271
ID ADE05106 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 272
ID ADD75319 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 273
ID ADD76863 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 274
ID ADD86631 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 275
ID ADE89239 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 276
ID ADE41199 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO337.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 277
ID ADD78099 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 278
ID ADE18378 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194794-A1.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 279
ID ADE88687 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 280
ID ADE89958 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FELY/) FELYAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMAADI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLMAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANT/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEM/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 281
ID ADD77607 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 282
ID ADD77853 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 283
ID ADD85311 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 284
ID ADD73843 standard; protein; 344 AA.
DE Human PRO polypeptide #63.

PN US2003100710-A1.
PD 23-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 285
ID ADD74581 standard; protein, 344 AA.
DE Human PRO polypeptide #63.
PN US2003100713-A1.
PD 23-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 286
ID ADD77109 standard; protein, 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100716-A1.
PD 23-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 287
ID ADD85603 standard; protein, 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100720-A1.
PD 23-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 288
ID ADE05352 standard; protein, 344 AA.
DE Human PRO polypeptide #63.
PN US2003100723-A1.
PD 23-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 289
ID ADD74627 standard; protein, 344 AA.
DE Human PRO polypeptide #63.
PN US2003100724-A1.
PD 23-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 290
ID ADF61598 standard; protein, 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 291
ID ADF40290 standard; protein, 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 292
ID ADF46086 standard; protein, 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 293
ID ADE94707 standard; protein, 344 AA.
DE Human PRO polypeptide #188.
PN US2003199027-A1.

PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 294
ID ADE91118 standard; protein, 344 AA.
DE Human PRO polypeptide #188.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 295
ID ADE95259 standard; protein, 344 AA.
DE Human PRO polypeptide #188.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 296
ID ADE93369 standard; protein, 344 AA.
DE Human PRO polypeptide #188.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 297
ID ADF24482 standard; protein, 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 298
ID ADF40914 standard; protein, 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 299
ID ADF23858 standard; protein, 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 300
ID ADF33841 standard; protein, 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 301
ID ADF34950 standard; protein, 344 AA.
DE Human PRO polypeptide #188.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 302
ID ADF27308 standard; protein, 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003199436-A1.
PD 23-OCT-2003.

PA	(GETH) GENENTECH INC.	100.0%;	Score 1806;	DB 8;	Length 344;
Query Match					
Best Local Similarity		100.0%;	Pred. No. 4.3e-147;		
RESULT 303					
ID	ADP72944 standard; protein; 344 AA.				
DE	Human secreted/transmembrane protein, PRO337.				
PN	US2003199437-A1.				
PD	23-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity		100.0%;	Pred. No. 4.3e-147;		
RESULT 304					
ID	ADP32265 standard; protein; 344 AA.				
DE	Novel human secreted and transmembrane protein PRO337.				
PN	US2003199051-A1.				
PD	23-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity		100.0%;	Pred. No. 4.3e-147;		
RESULT 305					
ID	ADP30566 standard; protein; 344 AA.				
DE	Human PRO polypeptide #188.				
PN	US2003199063-A1.				
PD	23-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity		100.0%;	Pred. No. 4.3e-147;		
RESULT 306					
ID	ADP41538 standard; protein; 344 AA.				
DE	Human secreted/transmembrane protein, PRO337.				
PN	US2003199435-A1.				
PD	23-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity		100.0%;	Pred. No. 4.3e-147;		
RESULT 307					
ID	ADP33217 standard; protein; 344 AA.				
DE	Human secreted/transmembrane protein, PRO337.				
PN	US2003211091-A1.				
PD	13-NOV-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity		100.0%;	Pred. No. 4.3e-147;		
RESULT 308					
ID	ADP25583 standard; protein; 344 AA.				
DE	Human secreted/transmembrane protein, PRO337.				
PN	US2003211092-A1.				
PD	13-NOV-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity		100.0%;	Pred. No. 4.3e-147;		
RESULT 309					
ID	ADP26684 standard; protein; 344 AA.				
DE	Human secreted/transmembrane protein, PRO337.				
PN	US2003199674-A1.				
PD	23-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity		100.0%;	Pred. No. 4.3e-147;		
RESULT 310					
ID	ADP34473 standard; protein; 344 AA.				
DE	Human secreted/transmembrane protein, PRO337.				
PN	US2003194410-A1.				
PD	16-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity		100.0%;	Pred. No. 4.3e-147;		
RESULT 311					
ID	ADP46710 standard; protein; 344 AA.				
DE	Human secreted/transmembrane protein, PRO337.				
PN	US2003195344-A1.				
PD	16-OCT-2003.				
PA	(GETH) GENENTECH INC.				

Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No.4.3e-147;		
RESULT 312				
ID	AD81713	standard; protein; 344 AA.		
DE	Novel human secreted and transmembrane protein PRO337.			
PN	US2003199058-A1.			
PD	23-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No.4.3e-147;		
RESULT 313				
ID	ADG05639	standard; protein; 344 AA.		
DE	Novel human secreted and transmembrane protein PRO337.			
PN	US2003096959-A1.			
PD	22-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No.4.3e-147;		
RESULT 314				
ID	ADG27193	standard; protein; 344 AA.		
DE	Human PRO polypeptide #63.			
PN	US2003096962-A1.			
PD	22-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No.4.3e-147;		
RESULT 315				
ID	ADG02292	standard; protein; 344 AA.		
DE	Human PRO polypeptide #188.			
PN	US2003207352-A1.			
PD	06-NOV-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No.4.3e-147;		
RESULT 316				
ID	ADG32078	standard; protein; 344 AA.		
DE	Novel human secreted and transmembrane protein PRO337.			
PN	US2003207360-A1.			
PD	06-NOV-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No.4.3e-147;		
RESULT 317				
ID	ADG20148	standard; protein; 344 AA.		
DE	Human PRO polypeptide #188.			
PN	US2003207376-A1.			
PD	06-NOV-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No.4.3e-147;		
RESULT 318				
ID	ADP98054	standard; protein; 344 AA.		
DE	Human PRO polypeptide #188.			
PN	US2003207422-A1.			
PD	06-NOV-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No.4.3e-147;		
RESULT 319				
ID	ADG24271	standard; protein; 344 AA.		
DE	Novel human secreted and transmembrane protein PRO337.			
PN	US2003207426-A1.			
PD	06-NOV-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No.4.3e-147;		
RESULT 320				
ID	ADP98625	standard; protein; 344 AA.		
DE	Human PRO polypeptide #188.			
PN	US2003208055-A1.			
PD	06-NOV-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No.4.3e-147;		
RESULT 321				
ID	ADG20148	standard; protein; 344 AA.		
DE	Human PRO polypeptide #188.			
PN	US2003207376-A1.			
PD	06-NOV-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No.4.3e-147;		
RESULT 322				
ID	ADG20148	standard; protein; 344 AA.		
DE	Human PRO polypeptide #188.			
PN	US2003207376-A1.			
PD	06-NOV-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No.4.3e-147;		
RESULT 323				
ID	ADG20148	standard; protein; 344 AA.		
DE	Human PRO polypeptide #188.			
PN	US2003207376-A1.			
PD	06-NOV-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No.4.3e-147;		
RESULT 324				
ID	ADG20148	standard; protein; 344 AA.		
DE	Human PRO polypeptide #188.			
PN	US2003207376-A1.			

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Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 321
ID ADG03456 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 322
ID ADP99177 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 323
ID ADG16762 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 324
ID ADG05221 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 325
ID ADG19488 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 326
ID ADG11256 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 327
ID ADG13325 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 328
ID ADG08382 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 329
ID ADG15552 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 330
ID ADG12035 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 331
ID ADP96950 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 332
ID ADG06135 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 333
ID ADG23719 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 334
ID ADG04008 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 335
ID ADG24909 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 336
ID ADP94592 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 337
ID ADG07206 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 338
ID ADG07758 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 339
ID ADG07758 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
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ID ADG06688 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 340
ID ADG55253 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 341
ID ADG60917 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 342
ID ADG62021 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 343
ID ADG82222 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 344
ID ADG57461 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 345
ID ADG56909 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 346
ID ADG55805 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 347
ID ADG58565 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 348
ID ADG70931 standard; protein; 344 AA.

DE Novel human secreted and transmembrane protein PRO337.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 349
ID ADH39032 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 350
ID ADG58013 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 351
ID ADG53597 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 352
ID ADG71483 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 353
ID ADG50696 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 354
ID ADG81670 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 355
ID ADH30632 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 356
ID ADG63634 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO337.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 357
ID ADH11999 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207419-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 358
ID ADG50072 standard; protein; 344 AA.
DE Human secreted/cranmembrane protein, PRO337.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 359
ID ADG51944 standard; protein; 344 AA.
DE Human secreted/cranmembrane protein, PRO337.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 360
ID ADG52421 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 361
ID ADG54449 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 362
ID ADG49448 standard; protein; 344 AA.
DE Human secreted/cranmembrane protein, PRO337.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 363
ID ADG81118 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 364
ID ADG56557 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 365
ID ADH12623 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 366
ID ADG48824 standard; protein; 344 AA.
DE Human secreted/cranmembrane protein, PRO337.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 367
ID ADG61469 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 368
ID ADH28556 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 369
ID ADG54701 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 370
ID ADG59741 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 371
ID ADG51320 standard; protein; 344 AA.
DE Human secreted/cranmembrane protein, PRO337.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 372
ID ADH43489 standard; protein; 344 AA.
DE Human PRO polypeptide #28.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 373
ID ADG59264 standard; protein; 344 AA.
DE Human secreted/cranmembrane protein, PRO337.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 374
ID ADG34122 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 375
ID ADG62720 standard; protein; 344 AA.
DE Human secreted/cranmembrane protein, PRO337.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 376
ID AD18165 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 377
ID AD133592 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 378
ID ADH69686 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 379
ID ADH25745 standard; protein; 344 AA.
DE Human PRO337 protein SEQ ID NO:523.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 380
ID ADG09908 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 381
ID AD115379 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 382
ID ADG09256 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 383
ID AD114711 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 384
ID AD129847 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
Query Match 100.0%; Score 1806; DB 8; Length 344;

Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 385
ID AD118306 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 386
ID ADM27244 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 387
ID ADJ63587 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 388
ID ADJ77482 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 389
ID ADK82834 standard; protein; 344 AA.
DE Human PRO polypeptide #28.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 390
ID ADK66602 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 391
ID ADJ65604 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 392
ID ADM27740 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 393
ID ADM17522 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;

RESULT 394
 ID ADL07356 standard; protein; 344 AA.
 DE Human secreted/cranemembrane protein, PRO337.
 PN US2004063921-A1.
 PD 01-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 395
 ID ADM42464 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2004058424-A1.
 PD 25-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 396
 ID ADM28326 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2004077064-A1.
 PD 22-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 397
 ID ADI95808 standard; protein; 344 AA.
 DE Human PRO polypeptide #188.
 PN US2003077659-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 398
 ID ADI96360 standard; protein; 344 AA.
 DE Novel human secreted and transmembrane protein PRO337.
 PN US2003207354-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1806; DB 8; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4.3e-147;
 RESULT 399
 ID AAM40499 standard; protein; 355 AA.
 DE Human polypeptide SEQ ID NO 5430.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 100.0%; Score 1806; DB 4; Length 355;
 Best Local Similarity 100.0%; Pred. No. 4.5e-147;
 RESULT 400
 ID ADI21580 standard; protein; 355 AA.
 DE Novel human polypeptide #59.
 PN WO2003025148-A2.
 PD 27-MAR-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 100.0%; Score 1806; DB 7; Length 355;
 Best Local Similarity 100.0%; Pred. No. 4.5e-147;
 RESULT 401
 ID AAB19722 standard; protein; 344 AA.
 DE Human SECK Clone 11753149, 0.37-encoded protein.
 PN WO200061754-A2.
 PD 19-OCT-2000.
 PA (CURA-) CURAGEN CORP.
 Query Match 99.6%; Score 1799; DB 3; Length 344;
 Best Local Similarity 99.7%; Pred. No. 1.7e-146;
 RESULT 402
 ID AAB19721 standard; protein; 344 AA.
 DE Human SECK Clone 11753149, 0.6-encoded protein.
 PN WO200061754-A2.
 PD 19-OCT-2000.
 PA (CURA-) CURAGEN CORP.
 Query Match 99.6%; Score 1799; DB 3; Length 344;
 Best Local Similarity 99.7%; Pred. No. 1.7e-146;
 RESULT 403

ID ADD18291 standard; protein; 344 AA.
 DE Human molecule (MOL) protein MOL11.
 PN WO2003003984-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 99.6%; Score 1799; DB 7; Length 344;
 Best Local Similarity 99.7%; Pred. No. 1.7e-146;
 RESULT 404
 ID ADD18289 standard; protein; 344 AA.
 DE Human molecule (MOL) protein MOL10.
 PN WO2003003984-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 99.6%; Score 1799; DB 7; Length 344;
 Best Local Similarity 99.7%; Pred. No. 1.7e-146;
 RESULT 405
 ID AAY41773 standard; protein; 343 AA.
 DE Human PRO337 protein sequence.
 PN WO9946281-A2.
 PD 16-SEP-1999.
 PA (GETH) GENENTECH INC.
 Query Match 99.2%; Score 1791.5; DB 2; Length 343;
 Best Local Similarity 99.7%; Pred. No. 7.7e-146;
 RESULT 406
 ID AAM38713 standard; protein; 344 AA.
 DE Human polypeptide SEQ ID NO 1858.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 92.2%; Score 1665.5; DB 4; Length 344;
 Best Local Similarity 95.2%; Pred. No. 5.7e-135;
 RESULT 407
 ID AAB20227 standard; protein; 344 AA.
 DE Human IG gene related protein SEQ ID NO 50.
 PN WO200299040-A2.
 PD 12-DEC-2002.
 PA (EXEL-) EXELIXIS INC.
 Query Match 92.2%; Score 1665.5; DB 6; Length 344;
 Best Local Similarity 95.2%; Pred. No. 5.7e-135;
 RESULT 408
 ID ABO56719 standard; protein; 344 AA.
 DE Lung cancer-associated polypeptide #312.
 PN WO200286443-A2.
 PD 31-OCT-2002.
 PA (BOSB-) BOS BIOTECHNOLOGY INC.
 Query Match 92.2%; Score 1665.5; DB 6; Length 344;
 Best Local Similarity 95.2%; Pred. No. 5.7e-135;
 RESULT 409
 ID ADG63209 standard; protein; 344 AA.
 DE Human neurotrophin protein.
 PN WO2003002765-A2.
 PD 09-JAN-2003.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 Query Match 92.2%; Score 1665.5; DB 7; Length 344;
 Best Local Similarity 95.2%; Pred. No. 5.7e-135;
 RESULT 410
 ID ADN39138 standard; protein; 344 AA.
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO.456.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (BOSB-) BOS BIOTECHNOLOGY INC.
 Query Match 92.2%; Score 1665.5; DB 7; Length 344;
 Best Local Similarity 95.2%; Pred. No. 5.7e-135;
 RESULT 411
 ID ADG63211 standard; protein; 355 AA.
 DE Human neurotrophin protein +33bp isoform.
 PN WO2003002765-A2.
 PD 09-JAN-2003.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 Query Match 91.4%; Score 1650; DB 7; Length 355;
 Best Local Similarity 92.2%; Pred. No. 1.3e-133;
 RESULT 412
 ID ADI35770 standard; protein; 355 AA.

DE Human neurotrophin.
 PN US2003100485-A1.
 PD 29-MAY-2003.
 PA (INCYTE) INCYTE GENOMICS INC.
 Query Match 91.4%; Score 1650; DB 7; Length 355;
 Best Local Similarity 92.2%; Pred. No. 1.3e-133;
 RESULT 413
 ID ADG63213 standard; protein; 367 AA.
 DE Human neurotrophin protein +69bp isoform.
 PN WO2003002765-A2.
 PD 09-JAN-2003.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 Query Match 91.0%; Score 1644; DB 7; Length 367;
 Best Local Similarity 89.1%; Pred. No. 4.5e-133;
 RESULT 414
 ID AAU79205 standard; protein; 381 AA.
 DE Human Kruppel associated DNA binding protein 42.
 PN WO200183541-A1.
 PD 08-NOV-2001.
 PA (SHAN-) SHANGHAI BIOWINDOM GENE DEV INC.
 Query Match 91.0%; Score 1643; DB 5; Length 381;
 Best Local Similarity 98.7%; Pred. No. 5.7e-133;
 RESULT 415
 ID AAY57602 standard; protein; 313 AA.
 DE Human protein SEQ ID NO:4.
 PN WO958668-A1.
 PD 18-NOV-1999.
 PA (ONOV) ONO PHARM CO LTD.
 Query Match 90.9%; Score 1642; DB 3; Length 313;
 Best Local Similarity 100.0%; Pred. No. 5.3e-133;
 RESULT 416
 ID ADI5772 standard; protein; 344 AA.
 DE Rat neurotrophin.
 PN US2003100485-A1.
 PD 29-MAY-2003.
 PA (INCYTE) INCYTE GENOMICS INC.
 Query Match 90.8%; Score 1639.5; DB 7; Length 344;
 Best Local Similarity 92.9%; Pred. No. 1e-132;
 RESULT 417
 ID ADG63215 standard; protein; 376 AA.
 DE Human neurotrophin protein +108bp isoform.
 PN WO2003002765-A2.
 PD 09-JAN-2003.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 Query Match 90.8%; Score 1639.5; DB 7; Length 376;
 Best Local Similarity 87.0%; Pred. No. 1.1e-132;
 RESULT 418
 ID ADE07928 standard; protein; 338 AA.
 DE Novel protein (useful for identifying genetic disorders) #83.
 PN WO2003058152-A2.
 PD 03-JUL-2003.
 PA (HYSR-) HYSRQ INC.
 Query Match 71.7%; Score 1295.5; DB 7; Length 338;
 Best Local Similarity 71.6%; Pred. No. 4.6e-103;
 RESULT 419
 ID ADO47380 standard; protein; 250 AA.
 DE Human neurotrophin-like protein-related rat neurotrophin protein SegID15.
 PN WO2004039942-A2.
 PD 13-MAY-2004.
 PA (NUVE-) NUVELO.
 Query Match 71.7%; Score 1295; DB 8; Length 250;
 Best Local Similarity 97.6%; Pred. No. 3.3e-103;
 RESULT 420
 ID ABJ20236 standard; protein; 345 AA.
 DE Human IG gene related protein SEQ ID NO 59.
 PN WO200299040-A2.
 PD 12-DEC-2002.
 PA (EXEL-) EXELIXIS INC.
 Query Match 70.2%; Score 1268; DB 6; Length 345;
 Best Local Similarity 71.2%; Pred. No. 1.1e-100;
 RESULT 421
 ID ADE83448 standard; protein; 345 AA.
 DE Human Protein Q14982, SEQ ID NO 11043.

PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 70.2%; Score 1268; DB 7; Length 345;
 Best Local Similarity 71.2%; Pred. No. 1.1e-100;
 RESULT 422
 ID ADG63207 standard; protein; 345 AA.
 DE Opioid-binding protein/cell adhesion molecule-like protein.
 PN WO2003002765-A2.
 PD 09-JAN-2003.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 Query Match 70.2%; Score 1266; DB 7; Length 345;
 Best Local Similarity 71.2%; Pred. No. 1.1e-100;
 RESULT 423
 ID ADE83446 standard; protein; 345 AA.
 DE Rat Protein P32736, SEQ ID NO 11041.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 69.7%; Score 1259; DB 7; Length 345;
 Best Local Similarity 71.2%; Pred. No. 6.6e-100;
 RESULT 424
 ID AAO16641 standard; protein; 335 AA.
 DE Human limbic system associated membrane protein 36-85.
 PN CN1345756-A.
 PD 24-APR-2002.
 PA (SHAN-) SHANGHAI BIOWINDOM GENE DEV INC.
 Query Match 51.6%; Score 932.5; DB 5; Length 335;
 Best Local Similarity 53.9%; Pred. No. 9.2e-72;
 RESULT 425
 ID ABJ20235 standard; protein; 338 AA.
 DE Human IG gene related protein SEQ ID NO 58.
 PN WO200299040-A2.
 PD 12-DEC-2002.
 PA (EXEL-) EXELIXIS INC.
 Query Match 51.6%; Score 931.5; DB 6; Length 338;
 Best Local Similarity 55.4%; Pred. No. 1.1e-71;
 RESULT 426
 ID ADL12675 standard; protein; 338 AA.
 DE Human steroid-induced C3A liver cell protein #60.
 PN US6673549-B1.
 PD 06-JAN-2004.
 PA (INCYTE) INCYTE CORP.
 Query Match 51.6%; Score 931.5; DB 8; Length 338;
 Best Local Similarity 55.4%; Pred. No. 1.1e-71;
 RESULT 427
 ID AAW05153 standard; protein; 338 AA.
 DE Rat LAMP residues 1-332.
 PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDNJ) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Query Match 51.3%; Score 926.5; DB 2; Length 338;
 Best Local Similarity 55.1%; Pred. No. 3.1e-71;
 RESULT 428
 ID AAW05154 standard; protein; 338 AA.
 DE Rat LAMP residues 1-332.
 PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDNJ) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Query Match 51.3%; Score 926; DB 2; Length 338;
 Best Local Similarity 55.1%; Pred. No. 3.1e-71;
 RESULT 429
 ID AAW05152 standard; protein; 325 AA.
 DE Human LAMP residues 8-332.
 PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDNJ) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Query Match 51.1%; Score 923.5; DB 2; Length 325;
 Best Local Similarity 55.3%; Pred. No. 5.3e-71;
 RESULT 430
 ID AAW05172 standard; protein; 361 AA.

DE Rat LAMP clone 6C.
 PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Query Match 50.6%; Score 913; DB 2; Length 361;
 Best Local Similarity 51.7%; Pred. No. 4.9e-70;
 RESULT 431
 ID AAW05157 standard; protein; 308 AA.
 DE Human LAMP residues 8-315.
 PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Query Match 50.3%; Score 908; DB 2; Length 308;
 Best Local Similarity 56.3%; Pred. No. 1.1e-69;
 RESULT 432
 ID AAW05158 standard; protein; 315 AA.
 DE Rat LAMP residues 1-315.
 PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Query Match 50.2%; Score 907; DB 2; Length 315;
 Best Local Similarity 56.3%; Pred. No. 1.3e-69;
 RESULT 433
 ID AAW05156 standard; protein; 310 AA.
 DE Rat mature LAMP.
 PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Query Match 50.1%; Score 905; DB 2; Length 310;
 Best Local Similarity 55.3%; Pred. No. 2e-69;
 RESULT 434
 ID AAW05155 standard; protein; 304 AA.
 DE Human mature LAMP.
 PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Query Match 49.9%; Score 902; DB 2; Length 304;
 Best Local Similarity 55.5%; Pred. No. 3.5e-69;
 RESULT 435
 ID ABR39441 standard; protein; 383 AA.
 DE Human GENSER peptide clone name SLAMP.
 PN WO2003014151-A2.
 PD 20-FEB-2003.
 PA (GENST) GENSET SA.
 Query Match 49.4%; Score 893; DB 6; Length 383;
 Best Local Similarity 53.3%; Pred. No. 2.8e-68;
 RESULT 436
 ID AAW05159 standard; protein; 287 AA.
 DE Human LAMP residues 29-315.
 PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Query Match 49.1%; Score 886.5; DB 2; Length 287;
 Best Local Similarity 56.6%; Pred. No. 6.9e-68;
 RESULT 437
 ID AAW05160 standard; protein; 287 AA.
 DE Rat LAMP residues 29-315.
 PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Query Match 49.0%; Score 885.5; DB 2; Length 287;
 Best Local Similarity 56.6%; Pred. No. 8.5e-68;
 RESULT 438
 ID ADM47275 standard; protein; 203 AA.
 DE Oestrogen regulated protein like NOVX 25b protein.
 PN WO2003083039-A2.
 PD 09-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 48.4%; Score 873.5; DB 7; Length 203;
 Best Local Similarity 54.5%; Pred. No. 5.7e-67;
 RESULT 439
 ID AAG75020 standard; protein; 326 AA.
 DE Human colon cancer antigen protein SEQ ID NO:5784.

PN WO200122920-A2.
 PD 05-APR-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 47.2%; Score 852.5; DB 4; Length 326;
 Best Local Similarity 51.6%; Pred. No. 7.1e-65;
 RESULT 440
 ID AAB31212 standard; protein; 354 AA.
 DE Amino acid sequence of human polypeptide PRO6004.
 PN WO200077037-A2.
 PD 21-DEC-2000.
 PA (GENTH) GENENTECH INC.
 Query Match 45.6%; Score 823; DB 4; Length 354;
 Best Local Similarity 47.9%; Pred. No. 2.8e-62;
 RESULT 441
 ID ABP53580 standard; protein; 354 AA.
 DE Human NOV12a protein SEQ ID NO:24.
 PN WO200262999-A2.
 PD 15-AUG-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 45.6%; Score 823; DB 5; Length 354;
 Best Local Similarity 47.9%; Pred. No. 2.8e-62;
 RESULT 442
 ID AAB3592 standard; protein; 354 AA.
 DE Human PRO protein, Seq ID No 2.
 PN WO200208288-A2.
 PD 31-JAN-2002.
 PA (GENTH) GENENTECH INC.
 Query Match 45.6%; Score 823; DB 5; Length 354;
 Best Local Similarity 47.9%; Pred. No. 2.8e-62;
 RESULT 443
 ID ADI28023 standard; protein; 354 AA.
 DE ECMCAD protein 7087904CD1.
 PN WO200202634-A2.
 PD 10-JAN-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 45.6%; Score 823; DB 5; Length 354;
 Best Local Similarity 47.9%; Pred. No. 2.8e-62;
 RESULT 444
 ID ABU80739 standard; protein; 354 AA.
 DE Human PRO polypeptide #1.
 PN US2003036635-A1.
 PD 20-FEB-2003.
 PA (GENTH) GENENTECH INC.
 Query Match 45.6%; Score 823; DB 6; Length 354;
 Best Local Similarity 47.9%; Pred. No. 2.8e-62;
 RESULT 445
 ID ABO25183 standard; protein; 354 AA.
 DE Novel human secreted and transmembrane protein PRO6004.
 PN US2003040014-A1.
 PD 27-FEB-2003.
 PA (GENTH) GENENTECH INC.
 Query Match 45.6%; Score 823; DB 6; Length 354;
 Best Local Similarity 47.9%; Pred. No. 2.8e-62;
 RESULT 446
 ID ABO33705 standard; protein; 354 AA.
 DE Novel human secreted and transmembrane protein PRO6004.
 PN US2003045687-A1.
 PD 06-MAR-2003.
 PA (GENTH) GENENTECH INC.
 Query Match 45.6%; Score 823; DB 6; Length 354;
 Best Local Similarity 47.9%; Pred. No. 2.8e-62;
 RESULT 447
 ID ABU67301 standard; protein; 354 AA.
 DE Novel human secreted and transmembrane protein PRO6004.
 PN US2003032063-A1.
 PD 13-FEB-2003.
 PA (GENTH) GENENTECH INC.
 Query Match 45.6%; Score 823; DB 6; Length 354;
 Best Local Similarity 47.9%; Pred. No. 2.8e-62;
 RESULT 448
 ID ABU72069 standard; protein; 354 AA.
 DE Novel human secreted and transmembrane protein PRO6004.
 PN US2002177165-A1.

PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 449
ID ABO617170 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 450
ID ABO82048 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 451
ID ABO79812 standard; protein; 354 AA.
DE Human secreted/transmembrane protein PRO6004.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 452
ID ABO72228 standard; protein; 354 AA.
DE Human PRO6004 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 453
ID ABO47302 standard; protein; 354 AA.
DE Human secreted/transmembrane polypeptide PRO6004.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 454
ID ABO72356 standard; protein; 354 AA.
DE Human PRO6004 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 455
ID ABO34251 standard; protein; 354 AA.
DE Human secreted/transmembrane polypeptide PRO 6004.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 6; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 456
ID ABO19870 standard; protein; 354 AA.
DE Human secreted/transmembrane protein PRO6004.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 457
ID ABO72058 standard; protein; 354 AA.
DE Human membrane bound receptor/protein PRO6004 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 458
ID ADB83492 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 459
ID ADB80598 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 460
ID ADB73139 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 461
ID ADB78221 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 462
ID ADB84869 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 463
ID ADB77975 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 464
ID ADB87041 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 465
ID ADB84623 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 466
ID ADB83738 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match	45.6%;	Score 823;	DB 7;	Length 354
Beet Local Similarity	47.9%;	Pred. No. 2.8e-62;		
RESULT 467				
ID AD672893 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003092887-A1.				
PD 15-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354
Beet Local Similarity	47.9%;	Pred. No. 2.8e-62;		
RESULT 468				
ID ADC66731 standard; protein; 354 AA.				
DE Human PRO polypeptide #1.				
FN US2003088065-A1.				
PD 08-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354
Beet Local Similarity	47.9%;	Pred. No. 2.8e-62;		
RESULT 469				
ID ADC21721 standard; protein; 354 AA.				
DE Human PRO polypeptide #1.				
FN US2003096969-A1.				
PD 22-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354
Beet Local Similarity	47.9%;	Pred. No. 2.8e-62;		
RESULT 470				
ID ADC49752 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003088064-A1.				
PD 08-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354
Beet Local Similarity	47.9%;	Pred. No. 2.8e-62;		
RESULT 471				
ID ADC48951 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003088070-A1.				
PD 08-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354
Beet Local Similarity	47.9%;	Pred. No. 2.8e-62;		
RESULT 472				
ID ADC49468 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003088071-A1.				
PD 08-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354
Beet Local Similarity	47.9%;	Pred. No. 2.8e-62;		
RESULT 473				
ID ADC47329 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003088072-A1.				
PD 08-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354
Beet Local Similarity	47.9%;	Pred. No. 2.8e-62;		
RESULT 474				
ID ADC47074 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003105288-A1.				
PD 05-JUN-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354
Beet Local Similarity	47.9%;	Pred. No. 2.8e-62;		
RESULT 475				
ID ADC77949 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003096972-A1.				
PD 22-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354
Beet Local Similarity	47.9%;	Pred. No. 2.8e-62;		
RESULT 476				
ID ADC77949 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003096972-A1.				
PD 22-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354
Beet Local Similarity	47.9%;	Pred. No. 2.8e-62;		
RESULT 477				
ID ADC77949 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003096972-A1.				
PD 22-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354
Beet Local Similarity	47.9%;	Pred. No. 2.8e-62;		
RESULT 478				
ID ADC77949 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003096972-A1.				
PD 22-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	45.6%;	Score 823;	DB 7;	Length 354
Beet Local Similarity	47.9%;	Pred. No. 2.8e-62;		
RESULT 479				
ID ADC77949 standard; protein; 354 AA.				
DE Novel human secreted and transmembrane protein PRO6004.				
FN US2003096972-A1.				
PD 22-MAY-2003.				
PA (GETH) GENENTECH INC.				

Best Local Similarity	47.9%;	Pred. No. 2.8e-62;
RESULT 476		
ID	ADD06194 standard; protein; 354 AA.	
DE	Novel human secreted and transmembrane protein PRO6004.	
PN	US20030731816-A1.	
PD	17-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	45.6%;	Score 823; DB 7; Length 354;
Best Local Similarity	47.9%;	Pred. No. 2.8e-62;
RESULT 477		
ID	ADC777003 standard; protein; 354 AA.	
DE	Novel human secreted and transmembrane protein PRO6004.	
PN	US200308066-A1.	
PD	08-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	45.6%;	Score 823; DB 7; Length 354;
Best Local Similarity	47.9%;	Pred. No. 2.8e-62;
RESULT 478		
ID	ADD50666 standard; protein; 354 AA.	
DE	Novel human secreted and transmembrane protein PRO6004.	
PN	US2003105291-A1.	
PD	05-JUN-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	45.6%;	Score 823; DB 7; Length 354;
Best Local Similarity	47.9%;	Pred. No. 2.8e-62;
RESULT 479		
ID	ADD50912 standard; protein; 354 AA.	
DE	Novel human secreted and transmembrane protein PRO6004.	
PN	US2003105290-A1.	
PD	05-JUN-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	45.6%;	Score 823; DB 7; Length 354;
Best Local Similarity	47.9%;	Pred. No. 2.8e-62;
RESULT 480		
ID	ADD50393 standard; protein; 354 AA.	
DE	Human PRO polypeptide #1.	
PN	US2003096971-A1.	
PD	22-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	45.6%;	Score 823; DB 7; Length 354;
Best Local Similarity	47.9%;	Pred. No. 2.8e-62;
RESULT 481		
ID	ADD50147 standard; protein; 354 AA.	
DE	Human PRO polypeptide #1.	
PN	US2003096970-A1.	
PD	22-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	45.6%;	Score 823; DB 7; Length 354;
Best Local Similarity	47.9%;	Pred. No. 2.8e-62;
RESULT 482		
ID	ADD51158 standard; protein; 354 AA.	
DE	Novel human secreted and transmembrane protein PRO6004.	
PN	US2003105289-A1.	
PD	05-JUN-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	45.6%;	Score 823; DB 7; Length 354;
Best Local Similarity	47.9%;	Pred. No. 2.8e-62;
RESULT 483		
ID	ADD63811 standard; protein; 354 AA.	
DE	Human secreted/transmembrane polypeptide PRO6004.	
PN	US2003170721-A1.	
PD	11-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	45.6%;	Score 823; DB 7; Length 354;
Best Local Similarity	47.9%;	Pred. No. 2.8e-62;
RESULT 484		
ID	ADC48705 standard; protein; 354 AA.	
DE	Novel human secreted and transmembrane protein PRO6004.	
PN	US2003092888-A1.	
PD	15-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	45.6%;	Score 823; DB 7; Length 354;
Best Local Similarity	47.9%;	Pred. No. 2.8e-62;
RESULT 485		
ID	ADD63811 standard; protein; 354 AA.	
DE	Novel human secreted and transmembrane protein PRO6004.	
PN	US2003092888-A1.	
PD	15-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	45.6%;	Score 823; DB 8; Length 354;
Best Local Similarity	47.9%;	Pred. No. 2.8e-62;

RESULT 485
ID ADE20876 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 486
ID ADE05720 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 487
ID ADD74949 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 488
ID ADD75695 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 489
ID ADD84927 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 490
ID ADD86753 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 491
ID ADE20630 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 492
ID ADE38927 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096362-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 493
ID ADE05474 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 494

ID ADD73459 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 495
ID ADD78299 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 496
ID ADE21122 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 497
ID ADD77237 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 498
ID ADE20384 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 499
ID ADD75449 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 500
ID ADD73965 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 501
ID ADD74211 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 502
ID ADD75941 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 503
ID ADD85433 standard; protein; 354 AA.

DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 504
ID ADB04982 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 505
ID ADD75195 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 506
ID ADD76739 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 507
ID ADB85607 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 508
ID ADB41225 standard; protein; 354 AA.
DE Human secreted/transmembrane polypeptide PRO6004.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 509
ID ADD77975 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 510
ID ADD77483 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 511
ID ADD77729 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 512
ID ADD85187 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 513
ID ADD73719 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 514
ID ADD74457 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 515
ID ADD76985 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 516
ID ADB85679 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 517
ID ADB05228 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 518
ID ADD74703 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 519
ID ADB05515 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 520
ID ADB27069 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 521
ID ADB1132 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096967-A1.

PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 522
ID ADG11911 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 523
ID ADF94468 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 524
ID ADG06564 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 525
ID ADH36908 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 526
ID ADG63659 standard; protein; 354 AA.
DE Human secreted/transmembrane polypeptide PRO6004.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 527
ID ADG33998 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2004006206-A1.
PD 08-JUN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 528
ID ADI33468 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 529
ID ADH69562 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 530
ID ADI23723 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096961-A1.
PD 22-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 531
ID ADM27120 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 532
ID ADK66478 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 533
ID ADS82050 standard; protein; 354 AA.
DE Human cancer-associated protein #5.
PN WO2004035789-A1.
PD 29-APR-2004.
PA (GLDS) LG LIFE SCI LTD.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 534
ID ABB96407 standard; protein; 354 AA.
DE Human NOV6, KILOM-like protein.
PN WO200255704-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
Query Match 45.5%; Score 822; DB 5; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 535
ID ADB64811 standard; protein; 354 AA.
DE Human protein encoded by clone OCBBP20110210.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELT-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 45.4%; Score 820; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 5e-62;
RESULT 536
ID ABB53581 standard; protein; 354 AA.
DE Human NOV12b protein SEQ ID NO:26.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 45.3%; Score 819; DB 5; Length 354;
Best Local Similarity 48.6%; Pred. No. 6.1e-62;
RESULT 537
ID ABJ20234 standard; protein; 348 AA.
DE Human IG gene related protein SEQ ID NO 57.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 45.1%; Score 815; DB 6; Length 348;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 538
ID ABJ20233 standard; protein; 348 AA.
DE Human IG gene related protein SEQ ID NO 56.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 45.1%; Score 815; DB 6; Length 348;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 539
ID ABA44331 standard; protein; 352 AA.
DE Human PRO4993 protein sequence SEQ ID NO:612.
PN WO200053756-A2.
PD 14-SEP-2000.

PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 3; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 540
ID ABO25277 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO4993.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 541
ID ABU72283 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO4993.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 542
ID ABU09489 standard; protein; 352 AA.
DE Human secreted and transmembrane PRO polypeptide #39.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 543
ID ABU61161 standard; protein; 352 AA.
DE Human PRO4993 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 544
ID ABU80430 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO4993.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 545
ID ADA25150 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO4993.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 546
ID ABO19732 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO4993.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 547
ID ADL12812 standard; protein; 352 AA.
DE Human secreted/transmembrane polypeptide PRO4993.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 6; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 548
ID ABO19623 standard; protein; 352 AA.
DE Novel human secreted and transmembrane polypeptide #91.
PN US2003049633-A1.
PD 13-MAR-2003.
Query Match 45.1%; Score 815; DB 6; Length 352;

Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 549
ID ADB74118 standard; protein; 352 AA.
DE Human PRO polypeptide #91.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 550
ID ADB76834 standard; protein; 352 AA.
DE Human PRO polypeptide #91.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 551
ID ADC44260 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 552
ID ADC62020 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 553
ID ADC63984 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 554
ID ADC67084 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 555
ID ADC69208 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 556
ID ADC63268 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 557
ID ADC68333 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;

RESULT 558
ID ADE41653 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 559
ID ADC67708 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 560
ID ADC62644 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 561
ID ADC42277 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 562
ID ADE49646 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 563
ID ADE35700 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 564
ID ADE16814 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 565
ID ADD73429 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 566
ID ADD72787 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 567

ID ADE17438 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 568
ID ADF47452 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 569
ID ADG53209 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 570
ID ADG60529 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 571
ID ADI61289 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 7; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 572
ID ADE48946 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 573
ID ADE90047 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLMAN K J.
PA (KLUJ/) KLUJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.

PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMA D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 574
ID ADF61687 standard; protein; 352 AA.
DE Human secreted/cranmembrane protein, PRO4993.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 575
ID ADF40379 standard; protein; 352 AA.
DE Human secreted/cranmembrane protein, PRO4993.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 576
ID ADF6175 standard; protein; 352 AA.
DE Human secreted/cranmembrane protein, PRO4993.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 577
ID ADF24571 standard; protein; 352 AA.
DE Human secreted/cranmembrane protein, PRO4993.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 578
ID ADF41003 standard; protein; 352 AA.
DE Human secreted/cranmembrane protein, PRO4993.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 579
ID ADF23947 standard; protein; 352 AA.
DE Human secreted/cranmembrane protein, PRO4993.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 580
ID ADF33930 standard; protein; 352 AA.
DE Human secreted/cranmembrane protein, PRO4993.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 581
ID ADF27397 standard; protein; 352 AA.
DE Human secreted/cranmembrane protein, PRO4993.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 582

ID ADF28033 standard; protein; 352 AA.
DE Human secreted/cranmembrane protein, PRO4993.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 583
ID ADF41627 standard; protein; 352 AA.
DE Human secreted/cranmembrane protein, PRO4993.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 584
ID ADF33306 standard; protein; 352 AA.
DE Human secreted/cranmembrane protein, PRO4993.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 585
ID ADF25672 standard; protein; 352 AA.
DE Human secreted/cranmembrane protein, PRO4993.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 586
ID ADF6773 standard; protein; 352 AA.
DE Human secreted/cranmembrane protein, PRO4993.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 587
ID ADF34562 standard; protein; 352 AA.
DE Human secreted/cranmembrane protein, PRO4993.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 588
ID ADF46799 standard; protein; 352 AA.
DE Human secreted/cranmembrane protein, PRO4993.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 589
ID ADF50785 standard; protein; 352 AA.
DE Human secreted/cranmembrane protein, PRO4993.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 590
ID ADF50161 standard; protein; 352 AA.
DE Human secreted/cranmembrane protein, PRO4993.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.1%; Score 815; DB 8; Length 352;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 591
ID ADF52033 standard; protein; 352 AA.

DE Human secreted/transmembrane protein, PRO4993.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;
RESULT 592
ID ADG49537 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;
RESULT 593
ID ADG48913 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;
RESULT 594
ID ADG51409 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;
RESULT 595
ID ADG59353 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;
RESULT 596
ID ADG62809 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;
RESULT 597
ID ADM17611 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;
RESULT 598
ID ADL07445 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO4993.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;
RESULT 599
ID AAM05167 standard; protein; 252 AA.
DE Human LAMP residues 46-294.
PN W096310052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match
Best Local Similarity 44.1%; Score 796.5; DB 2; Length 252;
RESULT 600
ID AAM05168 standard; protein; 252 AA.
DE Rat LAMP residues 46-294.

PN W096310052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match
Best Local Similarity 44.0%; Score 795.5; DB 2; Length 252;
RESULT 601
ID ABG96271 standard; protein; 336 AA.
DE Human immunoglobulin superfamily protein IGSPF-9.
PN W0200272794-A2.
PD 19-SEP-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 42.2%; Score 763; DB 5; Length 336;
RESULT 602
ID AAE29924 standard; protein; 336 AA.
DE Human LP289 protein.
PN W0200274906-A2.
PD 26-SEP-2002.
PA (ELIT) LILLY & CO ELI.
Query Match
Best Local Similarity 42.2%; Score 763; DB 6; Length 336;
RESULT 603
ID ADH71418 standard; protein; 336 AA.
DE Human protein of the invention NOV11q SEQ ID NO:314.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 42.2%; Score 763; DB 8; Length 336;
RESULT 604
ID ADH71412 standard; protein; 336 AA.
DE Human protein of the invention NOV11n SEQ ID NO:308.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 42.2%; Score 763; DB 8; Length 336;
RESULT 605
ID ADH71414 standard; protein; 336 AA.
DE Human protein of the invention NOV11o SEQ ID NO:310.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 42.2%; Score 763; DB 8; Length 336;
RESULT 606
ID ADH71388 standard; protein; 344 AA.
DE Human protein of the invention NOV11b SEQ ID NO:284.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 42.2%; Score 763; DB 8; Length 344;
RESULT 607
ID ADH71390 standard; protein; 325 AA.
DE Human protein of the invention NOV11c SEQ ID NO:286.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 42.2%; Score 762; DB 8; Length 325;
RESULT 608
ID AAE30252 standard; protein; 306 AA.
DE Human LP289 mature protein #1.
PN W0200274906-A2.
PD 26-SEP-2002.
PA (ELIT) LILLY & CO ELI.
Query Match
Best Local Similarity 42.1%; Score 761; DB 6; Length 306;
RESULT 609
ID ADH71402 standard; protein; 307 AA.
DE Human protein of the invention NOV11i SEQ ID NO:298.
PN W02003102155-A2.

PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.1%; Score 761; DB 8; Length 307;
 Best Local Similarity 52.5%; Pred. No. 5.1e-57;
 RESULT 610
 ID ADH71410 standard; protein; 309 AA.
 DE Human protein of the invention NOV11m SEQ ID NO:306.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.1%; Score 761; DB 8; Length 309;
 Best Local Similarity 52.5%; Pred. No. 5.1e-57;
 RESULT 611
 ID ADH71406 standard; protein; 309 AA.
 DE Human protein of the invention NOV11k SEQ ID NO:302.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.1%; Score 761; DB 8; Length 309;
 Best Local Similarity 52.5%; Pred. No. 5.1e-57;
 RESULT 612
 ID AAE30253 standard; protein; 314 AA.
 DE Human LP289 mature protein #2.
 PN WO200274906-A2.
 PD 26-SEP-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 42.1%; Score 761; DB 6; Length 314;
 Best Local Similarity 52.5%; Pred. No. 5.3e-57;
 RESULT 613
 ID ADH71394 standard; protein; 315 AA.
 DE Human protein of the invention NOV11e SEQ ID NO:290.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.1%; Score 761; DB 8; Length 315;
 Best Local Similarity 52.5%; Pred. No. 5.3e-57;
 RESULT 614
 ID ABG94637 standard; protein; 319 AA.
 DE Human NOV5b protein.
 PN WO200266643-A2.
 PD 29-AUG-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.1%; Score 761; DB 5; Length 319;
 Best Local Similarity 52.5%; Pred. No. 5.4e-57;
 RESULT 615
 ID ABG94636 standard; protein; 319 AA.
 DE Human NOV5a protein.
 PN WO200266643-A2.
 PD 29-AUG-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.1%; Score 761; DB 5; Length 319;
 Best Local Similarity 52.5%; Pred. No. 5.4e-57;
 RESULT 616
 ID ADL35977 standard; protein; 319 AA.
 DE Human NOVX polypeptide #11.
 PN US2003207800-A1.
 PD 06-NOV-2003.
 PA (MALY) MALYANKAR U M.
 (SHEN) SHENOY S G.
 (SPYT) SPYTEK K A.
 (ZERH) ZERHUSEN B D.
 (PATY) PATURAJAN M.
 (GUOX) GUO X.
 (KEKU) KEKUDA R.
 (GANG) GANGOLI E A.
 (SHIM) SHIMKETS R A.
 (TAUP) TAUPIER R J.
 (LIL/) LI L.
 (PADI) PADIGARU M.
 Query Match 42.1%; Score 761; DB 7; Length 319;
 Best Local Similarity 52.5%; Pred. No. 5.4e-57;
 RESULT 617
 ID ADL35979 standard; protein; 319 AA.

DE Human NOVX polypeptide #12.
 PN US2003207800-A1.
 PD 06-NOV-2003.
 PA (MALY) MALYANKAR U M.
 (SHEN) SHENOY S G.
 (SPYT) SPYTEK K A.
 (ZERH) ZERHUSEN B D.
 (PATY) PATURAJAN M.
 (GUOX) GUO X.
 (KEKU) KEKUDA R.
 (GANG) GANGOLI E A.
 (SHIM) SHIMKETS R A.
 (TAUP) TAUPIER R J.
 (LIL/) LI L.
 (PADI) PADIGARU M.
 Query Match 42.1%; Score 761; DB 7; Length 319;
 Best Local Similarity 52.5%; Pred. No. 5.4e-57;
 RESULT 618
 ID ADH71400 standard; protein; 319 AA.
 DE Human protein of the invention NOV11h SEQ ID NO:296.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.1%; Score 761; DB 8; Length 319;
 Best Local Similarity 52.5%; Pred. No. 5.4e-57;
 RESULT 619
 ID ADH71396 standard; protein; 319 AA.
 DE Human protein of the invention NOV11f SEQ ID NO:292.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.1%; Score 761; DB 8; Length 319;
 Best Local Similarity 52.5%; Pred. No. 5.4e-57;
 RESULT 620
 ID ADH71416 standard; protein; 320 AA.
 DE Human protein of the invention NOV11g SEQ ID NO:312.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.1%; Score 761; DB 8; Length 320;
 Best Local Similarity 52.5%; Pred. No. 5.4e-57;
 RESULT 621
 ID ADH71398 standard; protein; 325 AA.
 DE Human protein of the invention NOV11g SEQ ID NO:294.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.1%; Score 761; DB 8; Length 325;
 Best Local Similarity 52.5%; Pred. No. 5.5e-57;
 RESULT 622
 ID ADH71422 standard; protein; 336 AA.
 DE Human protein of the invention NOV11s SEQ ID NO:318.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.1%; Score 760; DB 8; Length 336;
 Best Local Similarity 50.6%; Pred. No. 7e-57;
 RESULT 623
 ID ADH71386 standard; protein; 336 AA.
 DE Human protein of the invention NOV11a SEQ ID NO:282.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 42.1%; Score 760; DB 8; Length 336;
 Best Local Similarity 50.6%; Pred. No. 7e-57;
 RESULT 624
 ID ABG94638 standard; protein; 307 AA.
 DE Human NOV5c protein.
 PN WO200266643-A2.
 PD 29-AUG-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 41.9%; Score 757; DB 5; Length 307;
 Best Local Similarity 52.5%; Pred. No. 1.1e-56;

RESULT 625
ID ADH71404 standard; protein; 319 AA.
DE Human protein of the invention NOV11j SEQ ID NO:300.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 41.9%; Score 757; DB 8; Length 319;
Best Local Similarity 52.5%; Pred. No. 1.2e-56;
RESULT 626
ID ADH71420 standard; protein; 336 AA.
DE Human protein of the invention NOV11j SEQ ID NO:316.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 41.9%; Score 757; DB 8; Length 336;
Best Local Similarity 50.3%; Pred. No. 1.3e-56;
RESULT 627
ID ADP2916 standard; protein; 278 AA.
DE Human secreted protein SEQ ID #683.
PN W02004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 41.7%; Score 752.5; DB 8; Length 278;
Best Local Similarity 54.1%; Pred. No. 2.4e-56;
RESULT 628
ID AAE30254 standard; protein; 284 AA.
DE Human LP289 mature protein #3.
PN W0200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 41.7%; Score 752.5; DB 6; Length 284;
Best Local Similarity 54.1%; Pred. No. 2.5e-56;
RESULT 629
ID AAE30256 standard; protein; 291 AA.
DE Human LP289 mature protein #5.
PN W0200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 41.7%; Score 752.5; DB 6; Length 291;
Best Local Similarity 54.1%; Pred. No. 2.6e-56;
RESULT 630
ID AAE30255 standard; protein; 292 AA.
DE Human LP289 mature protein #4.
PN W0200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 41.7%; Score 752.5; DB 6; Length 292;
Best Local Similarity 54.1%; Pred. No. 2.6e-56;
RESULT 631
ID ADL35981 standard; protein; 305 AA.
DE Human NOVX polypeptide #13.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY) MALYANKAR U M.
PA (SHEN) SHENOY S G.
PA (SPYT) SPYTEK K A.
PA (ZERH) ZERHUSEN B D.
PA (PATR) PATURAJAN M.
PA (GUOX) GUO X.
PA (KEKU) KEKUDA R.
PA (GANG) GANGOLLI E A.
PA (SHIM) SHIMKETS R A.
PA (TAUP) TAUPIER R J.
PA (LILJ) LI L.
PA (PADJ) PADIGARU M.
Query Match 40.3%; Score 727; DB 7; Length 305;
Best Local Similarity 51.8%; Pred. No. 4.3e-54;
RESULT 632
ID AAU84386 standard; protein; 336 AA.
DE Novel human secreted or membrane-associated protein #25.
PN W0200204600-A2.
PD 17-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 40.2%; Score 726; DB 5; Length 336;
Best Local Similarity 50.5%; Pred. No. 6e-54;
RESULT 633
ID ABG94639 standard; protein; 336 AA.
DE Human NOV5d protein.
PN W0200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 39.9%; Score 721; DB 5; Length 336;
Best Local Similarity 50.5%; Pred. No. 1.6e-53;
RESULT 634
ID ADH71408 standard; protein; 336 AA.
DE Human protein of the invention NOV11j SEQ ID NO:304.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 39.9%; Score 721; DB 8; Length 336;
Best Local Similarity 50.5%; Pred. No. 1.6e-53;
RESULT 635
ID ABB10253 standard; protein; 281 AA.
DE Human cDNA SEQ ID NO: 561.
PN W0200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.9%; Score 720.5; DB 4; Length 281;
Best Local Similarity 50.4%; Pred. No. 1.4e-53;
RESULT 636
ID ABP66840 standard; protein; 281 AA.
DE Human polypeptide SEQ ID NO 561.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE) ROSEN C A.
PA (RUBE) RUBEN S M.
PA (BARA) BARASH S C.
Query Match 39.9%; Score 720.5; DB 5; Length 281;
Best Local Similarity 50.4%; Pred. No. 1.4e-53;
RESULT 637
ID ADL35983 standard; protein; 336 AA.
DE Human NOVX polypeptide #14.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY) MALYANKAR U M.
PA (SHEN) SHENOY S G.
PA (SPYT) SPYTEK K A.
PA (ZERH) ZERHUSEN B D.
PA (PATR) PATURAJAN M.
PA (GUOX) GUO X.
PA (KEKU) KEKUDA R.
PA (GANG) GANGOLLI E A.
PA (SHIM) SHIMKETS R A.
PA (TAUP) TAUPIER R J.
PA (LILJ) LI L.
PA (PADJ) PADIGARU M.
Query Match 39.4%; Score 712; DB 7; Length 336;
Best Local Similarity 50.2%; Pred. No. 9.7e-53;
RESULT 638
ID ADH71392 standard; protein; 253 AA.
DE Human protein of the invention NOV11d SEQ ID NO:288.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.1%; Score 687.5; DB 8; Length 253;
Best Local Similarity 55.6%; Pred. No. 8.5e-51;
RESULT 639
ID AAU84385 standard; protein; 351 AA.
DE Novel human secreted or membrane-associated protein #24.
PN W0200204600-A2.
PD 17-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.

Query Match 37.7%; Score 681.5; DB 5; Length 351;
 Best Local Similarity 50.7%; Pred. No. 4.4e-50;
 RESULT 640
 ID ABE13848 standard; protein: 141 AA.
 DE Novel human diagnostic protein #13839.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 33.4%; Score 603; DB 4; Length 141;
 Best Local Similarity 86.6%; Pred. No. 7.5e-44;
 RESULT 641
 ID AAE30271 standard; protein: 294 AA.
 DE Human LP319b protein variant #2.
 PN WO200274906-A2.
 PD 26-SEP-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 33.4%; Score 603; DB 6; Length 294;
 Best Local Similarity 45.0%; Pred. No. 2e-43;
 RESULT 642
 ID AAE30270 standard; protein: 286 AA.
 DE Human LP319b protein variant #1.
 PN WO200274906-A2.
 PD 26-SEP-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 33.2%; Score 600; DB 6; Length 286;
 Best Local Similarity 45.0%; Pred. No. 3.6e-43;
 RESULT 643
 ID ADP29917 standard; protein: 222 AA.
 DE Human secreted protein SEQ ID #684.
 PN WO2004035732-A2.
 PD 29-APR-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 33.2%; Score 599.5; DB 8; Length 222;
 Best Local Similarity 54.0%; Pred. No. 2.8e-43;
 RESULT 644
 ID ABE13447 standard; protein: 130 AA.
 DE Novel human diagnostic protein #13838.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 31.5%; Score 569.5; DB 4; Length 130;
 Best Local Similarity 88.9%; Pred. No. 5.2e-41;
 RESULT 645
 ID AAE30269 standard; protein: 234 AA.
 DE Human LP319b protein mature sequence #2.
 PN WO200274906-A2.
 PD 26-SEP-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 29.2%; Score 527; DB 6; Length 234;
 Best Local Similarity 53.2%; Pred. No. 5.4e-37;
 RESULT 646
 ID AAE29927 standard; protein: 256 AA.
 DE Human LP319b protein.
 PN WO200274906-A2.
 PD 26-SEP-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 29.2%; Score 527; DB 6; Length 256;
 Best Local Similarity 53.2%; Pred. No. 6.1e-37;
 RESULT 647
 ID ABE13816 standard; protein: 872 AA.
 DE Novel human diagnostic protein #13807.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 29.1%; Score 525.5; DB 4; Length 872;
 Best Local Similarity 43.4%; Pred. No. 4.4e-36;
 RESULT 648
 ID ADE08994 standard; protein: 872 AA.
 DE Novel protein-related config polypeptide sequence #60.
 PN WO2003054152-A2.
 PD 03-JUN-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 29.1%; Score 525.5; DB 7; Length 872;

Best Local Similarity 43.4%; Pred. No. 4.4e-36;
 RESULT 649
 ID AAE30268 standard; protein: 226 AA.
 DE Human LP319b protein mature sequence #1.
 PN WO200274906-A2.
 PD 26-SEP-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 28.0%; Score 505; DB 6; Length 226;
 Best Local Similarity 53.0%; Pred. No. 4e-35;
 RESULT 650
 ID AAE30264 standard; protein: 211 AA.
 DE Human LP319a protein mature sequence #1.
 PN WO200274906-A2.
 PD 26-SEP-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 26.1%; Score 472; DB 6; Length 211;
 Best Local Similarity 54.1%; Pred. No. 2.6e-32;
 RESULT 651
 ID AAE30265 standard; protein: 222 AA.
 DE Human LP319a protein mature sequence #2.
 PN WO200274906-A2.
 PD 26-SEP-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 26.1%; Score 472; DB 6; Length 222;
 Best Local Similarity 54.1%; Pred. No. 2.8e-32;
 RESULT 652
 ID AAE29926 standard; protein: 241 AA.
 DE Human LP319a protein.
 PN WO200274906-A2.
 PD 26-SEP-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 26.1%; Score 472; DB 6; Length 241;
 Best Local Similarity 54.1%; Pred. No. 3.1e-32;
 RESULT 653
 ID ABB69485 standard; protein: 413 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 35247.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 18.7%; Score 338.5; DB 4; Length 413;
 Best Local Similarity 28.0%; Pred. No. 2.1e-20;
 RESULT 654
 ID ABB65642 standard; protein: 315 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 23718.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 18.4%; Score 333; DB 4; Length 315;
 Best Local Similarity 31.9%; Pred. No. 4.4e-20;
 RESULT 655
 ID ABB62574 standard; protein: 545 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 14514.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 16.9%; Score 306; DB 4; Length 545;
 Best Local Similarity 28.9%; Pred. No. 2e-17;
 RESULT 656
 ID ABB58947 standard; protein: 333 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 3633.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 16.5%; Score 297.5; DB 4; Length 333;
 Best Local Similarity 29.7%; Pred. No. 5.4e-17;
 RESULT 657
 ID ADS10483 standard; protein: 2537 AA.
 DE Human therapeutic protein - SEQ ID 720.
 PN WO2004080148-A2.
 PD 23-SEP-2004.
 PA (NOVE-) NOVELO INC.
 Query Match 16.1%; Score 290.5; DB 8; Length 2537;
 Best Local Similarity 29.8%; Pred. No. 3.5e-15;

RESULT 658
ID ABU12083 standard; protein; 2572 AA.
DE Human NOV25b CG93858-02 protein SEQ ID 86.
PN W0200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.1%; Score 290.5; DB 6; Length 2572;
Best Local Similarity 29.8%; Pred. No. 3.6e-15;
RESULT 659
ID ADK60225 standard; protein; 2673 AA.
DE Angiogenesis differentially expressed protein GS-P52.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 16.1%; Score 290.5; DB 8; Length 2673;
Best Local Similarity 29.8%; Pred. No. 3.8e-15;
RESULT 660
ID ADK60526 standard; protein; 2673 AA.
DE Angiogenesis differentially expressed protein GS-P52.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 16.1%; Score 290.5; DB 8; Length 2673;
Best Local Similarity 29.8%; Pred. No. 3.8e-15;
RESULT 661
ID ADP73149 standard; protein; 2673 AA.
DE Angiogenesis inhibitor human protein sequence, GS-P52.
PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE-) GENE S.
PA (ALMS/) AL M S.
Query Match 16.1%; Score 290.5; DB 8; Length 2673;
Best Local Similarity 29.8%; Pred. No. 3.8e-15;
RESULT 662
ID ABU69135 standard; protein; 4495 AA.
DE Human NOVX polypeptide #10.
PN W0200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.1%; Score 290.5; DB 6; Length 4495;
Best Local Similarity 29.8%; Pred. No. 7.7e-15;
RESULT 663
ID ADH72106 standard; protein; 4495 AA.
DE Human protein of the invention NOV43c SEQ ID NO:1002.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 16.1%; Score 290.5; DB 8; Length 4495;
Best Local Similarity 29.8%; Pred. No. 7.7e-15;
RESULT 664
ID ADO08273 standard; protein; 4495 AA.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LITX/) LIT X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.

PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATI/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHINKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERR/) ZERHUSEN B D.
Query Match 16.1%; Score 290.5; DB 8; Length 4495;
Best Local Similarity 29.8%; Pred. No. 7.7e-15;
RESULT 665
ID ADJ70089 standard; protein; 5636 AA.
DE Human heart mitochondrial protein as a therapeutic target SeqID1895.
PN W02003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 16.1%; Score 290.5; DB 7; Length 5636;
Best Local Similarity 31.1%; Pred. No. 1e-14;
RESULT 666
ID ADJ83137 standard; protein; 5636 AA.
DE Human hemiscitin protein - SEQ ID 128.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEY V T.
PA (LITX/) LIT X.
PA (SPYT/) SPYTEK K A.
PA (ZERR/) ZERHUSEN B D.
PA (PATI/) PATTURAJAN M.
PA (LEPL/) LEPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHINKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 16.1%; Score 290.5; DB 7; Length 5636;
Best Local Similarity 31.1%; Pred. No. 1e-14;
RESULT 667
ID ADK60205 standard; protein; 5636 AA.
DE Angiogenesis differentially expressed protein GS-P29.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 16.1%; Score 290.5; DB 8; Length 5636;
Best Local Similarity 31.1%; Pred. No. 1e-14;
RESULT 668
ID ADK60506 standard; protein; 5636 AA.
DE Angiogenesis differentially expressed protein GS-P29.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 16.1%; Score 290.5; DB 8; Length 5636;

Best Local Similarity 31.1%; Pred. No. 1e-14;
 RESULT 669
 ID ADP73129 standard; protein; 5636 AA.
 DE Angiogenesis inhibitor human protein sequence, GS-P29.
 PN FR2843753-A1.
 PD 27-FEB-2004.
 PA (GENE/) GENE S.
 PA (ALMS/) AL M S.
 Query Match
 Best Local Similarity 31.1%; Score 290.5; DB 8; Length 5636;
 RESULT 670
 ID ADG39844 standard; protein; 1708 AA.
 DE Protein similar to human NOV9 #5.
 PN US2003203843-A1.
 PD 30-OCT-2003.
 PA (PENA/) PENA C E A.
 PA (GUOX/) GUO X.
 PA (SHIM/) SHIMKETS R A.
 PA (PADI/) PADIGARU M.
 PA (KEKU/) KEKUDA R.
 PA (SEYT/) SEYTEK K A.
 PA (MEHR/) MEHRABAN F.
 PA (TOPP/) TOPPER J N.
 PA (MALY/) MALYANKAR U M.
 PA (WASS/) WASSERMAN S M.
 PA (EDIN/) EDINGER S R.
 PA (SMIT/) SMITHSON G.
 PA (GUNT/) GUNTHER E.
 PA (KOMU/) KOMUVES L.
 Query Match
 Best Local Similarity 16.0%; Score 289.5; DB 7; Length 1708;
 RESULT 671
 ID ADG39840 standard; protein; 1708 AA.
 DE Protein similar to human NOV9 #1.
 PN US2003203843-A1.
 PD 30-OCT-2003.
 PA (PENA/) PENA C E A.
 PA (GUOX/) GUO X.
 PA (SHIM/) SHIMKETS R A.
 PA (PADI/) PADIGARU M.
 PA (KEKU/) KEKUDA R.
 PA (SEYT/) SEYTEK K A.
 PA (MEHR/) MEHRABAN F.
 PA (TOPP/) TOPPER J N.
 PA (MALY/) MALYANKAR U M.
 PA (WASS/) WASSERMAN S M.
 PA (EDIN/) EDINGER S R.
 PA (SMIT/) SMITHSON G.
 PA (GUNT/) GUNTHER E.
 PA (KOMU/) KOMUVES L.
 Query Match
 Best Local Similarity 16.0%; Score 289.5; DB 7; Length 1708;
 RESULT 672
 ID ADG39840 standard; protein; 1708 AA.
 DE Protein similar to human NOV9 #1.
 PN US2003203843-A1.
 PD 30-OCT-2003.
 PA (PENA/) PENA C E A.
 PA (GUOX/) GUO X.
 PA (SHIM/) SHIMKETS R A.
 PA (PADI/) PADIGARU M.
 PA (KEKU/) KEKUDA R.
 PA (SEYT/) SEYTEK K A.
 PA (MEHR/) MEHRABAN F.
 PA (TOPP/) TOPPER J N.
 PA (MALY/) MALYANKAR U M.
 PA (WASS/) WASSERMAN S M.
 PA (EDIN/) EDINGER S R.
 PA (SMIT/) SMITHSON G.
 PA (GUNT/) GUNTHER E.
 PA (KOMU/) KOMUVES L.
 Query Match
 Best Local Similarity 16.0%; Score 289.5; DB 7; Length 1708;
 RESULT 673
 ID ADH72102 standard; protein; 707 AA.
 DE Human protein of the invention NOV43a SEQ ID NO:998.
 PN WO2003102155-A2.
 PD 14-NOV-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 16.0%; Score 288.5; DB 6; Length 707;
 RESULT 674
 ID ADH72102 standard; protein; 707 AA.
 DE Human protein of the invention NOV43a SEQ ID NO:998.
 PN WO2003102155-A2.
 PD 14-NOV-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 16.0%; Score 288.5; DB 6; Length 707;
 RESULT 675
 ID ADH72104 standard; protein; 712 AA.
 DE Human protein of the invention NOV43b SEQ ID NO:1000.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 16.0%; Score 288.5; DB 8; Length 707;
 RESULT 676
 ID ABU99129 standard; protein; 961 AA.
 DE Novel human GPCR related protein NOV9b.
 PN WO200299116-A2.
 PD 12-DEC-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 16.0%; Score 288.5; DB 6; Length 961;
 RESULT 677
 ID ADM93823 standard; protein; 961 AA.
 DE Human NOV protein #21.
 PN US2004009480-A1.
 PD 15-JAN-2004.
 PA (ANDE/) ANDERSON D W.
 PA (BAUM/) BAUMGARTNER J C.
 PA (BOLD/) BOLDIG F L.
 PA (CASW/) CASMAN S J.
 PA (EDIN/) EDINGER S R.
 PA (GANG/) GANGEOLI E A.
 PA (GERL/) GERLACH V.
 PA (GORM/) GORMAN L.
 PA (GUOX/) GUO X S.
 PA (HJAL/) HJALT T.
 PA (KEKU/) KEKUDA R.
 PA (LILU/) LI L.
 PA (MACD/) MACDOUGALL J R.
 PA (MALY/) MALYANKAR U M.
 PA (MILT/) MILLET I.
 PA (PADI/) PADIGARU M.
 PA (PATU/) PATTURAJAN M.
 PA (PENA/) PENA C E A.
 PA (RAST/) RASTELLI L.
 PA (SHIM/) SHIMKETS R A.
 PA (STON/) STONE D J.

PA (ALSO/) ALSOBROOK J P.
 PA (ANDE/) ANDERSON D W.
 PA (BOLD/) BOLDIG F L.
 PA (BURG/) BURGESS C E.
 PA (CASW/) CASMAN S J.
 PA (CHAP/) CHAPOVAL A.
 PA (EDIN/) EDINGER S R.
 PA (GERL/) GERLACH V.
 PA (GORM/) GORMAN L.
 PA (GUNT/) GUNTHER E.
 PA (GUOX/) GUO X S.
 PA (KEKU/) KEKUDA R.
 PA (LEPL/) LEFLEY D M.
 PA (LILU/) LI L.
 PA (LITX/) LIU X.
 PA (MALY/) MALYANKAR U M.
 PA (MILT/) MILLER C E.
 PA (MILT/) MILLER I.
 PA (PADI/) PADIGARU M.
 PA (PATU/) PATTURAJAN M.
 PA (PENA/) PENA C E A.
 PA (RIEG/) RIEGER D K.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (SEYT/) SEYTEK K A.
 PA (TAUP/) TAUPIER R J.
 PA (VERN/) VERNET C A M.
 PA (VOSS/) VOSS E Z.
 PA (ZERR/) ZERRHUSEN B D.
 Query Match
 Best Local Similarity 16.0%; Score 288.5; DB 8; Length 707;
 RESULT 675
 ID ADH72104 standard; protein; 712 AA.
 DE Human protein of the invention NOV43b SEQ ID NO:1000.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 16.0%; Score 288.5; DB 8; Length 712;
 RESULT 676
 ID ABU99129 standard; protein; 961 AA.
 DE Novel human GPCR related protein NOV9b.
 PN WO200299116-A2.
 PD 12-DEC-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 16.0%; Score 288.5; DB 6; Length 961;
 RESULT 677
 ID ADM93823 standard; protein; 961 AA.
 DE Human NOV protein #21.
 PN US2004009480-A1.
 PD 15-JAN-2004.
 PA (ANDE/) ANDERSON D W.
 PA (BAUM/) BAUMGARTNER J C.
 PA (BOLD/) BOLDIG F L.
 PA (CASW/) CASMAN S J.
 PA (EDIN/) EDINGER S R.
 PA (GANG/) GANGEOLI E A.
 PA (GERL/) GERLACH V.
 PA (GORM/) GORMAN L.
 PA (GUOX/) GUO X S.
 PA (HJAL/) HJALT T.
 PA (KEKU/) KEKUDA R.
 PA (LILU/) LI L.
 PA (MACD/) MACDOUGALL J R.
 PA (MALY/) MALYANKAR U M.
 PA (MILT/) MILLER I.
 PA (PADI/) PADIGARU M.
 PA (PATU/) PATTURAJAN M.
 PA (PENA/) PENA C E A.
 PA (RAST/) RASTELLI L.
 PA (SHIM/) SHIMKETS R A.
 PA (STON/) STONE D J.

PA (SPYT/) SPYTEK K A.
 PA (VERN/) VERNET C A M.
 PA (VOSS/) VOSS E Z.
 PA (ZERR/) ZERHUSEN B D.
 Query Match
 Best Local Similarity 16.0%; Score 288.5; DB 8; Length 961;
 RESULT 678
 ID ABB03933 standard; protein; 1240 AA.
 DE Novel human diagnostic protein #3924.
 PN W0200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 16.0%; Score 288.5; DB 4; Length 1240;
 RESULT 679
 ID AAB47771 standard; protein; 1336 AA.
 DE Human thrombospondin protein, BTL.012.
 PN W0200174852-A2.
 PD 11-OCT-2001.
 PA (FARB) BAYER CORP.
 Query Match
 Best Local Similarity 16.0%; Score 288.5; DB 5; Length 1336;
 RESULT 680
 ID ABB12084 standard; protein; 1902 AA.
 DE Human NOV25c CG56914-03 protein SEQ ID 88.
 PN W0200281625-A2.
 PD 17-OCT-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 16.0%; Score 288.5; DB 6; Length 1902;
 RESULT 681
 ID ABB72108 standard; protein; 1902 AA.
 DE Human protein of the invention NOV43d SEQ ID NO:1004.
 PN W02003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 16.0%; Score 288.5; DB 8; Length 1902;
 RESULT 682
 ID ABB16058 standard; protein; 1953 AA.
 DE G-coupled protein receptor related polypeptide, SEQ ID No 88.
 PN W0200283841-A2.
 PD 24-OCT-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 16.0%; Score 288.5; DB 7; Length 1953;
 RESULT 683
 ID ABB93997 standard; protein; 1953 AA.
 DE Human G-coupled protein receptor-related protein #44.
 PN US2004006205-A1.
 PD 08-JAN-2004.
 PA (LILU/) LI L.
 PA (GERL/) GERLACH V.
 PA (LIUX/) LIU X.
 PA (MILK/) MILNER C E.
 PA (SPYT/) SPYTEK K A.
 PA (ZERR/) ZERHUSEN B D.
 PA (PENNA) PENNA C E A.
 PA (SHEN/) SHENOY S G.
 PA (ZHON/) ZHONG H.
 PA (SMIT/) SMITHSON G.
 PA (CASW/) CASMAN S J.
 PA (BOLD/) BOLDOG F L.
 PA (VOSS/) VOSS E Z.
 PA (VERN/) VERNET C A.
 PA (MACD/) MACDOUGALL J R.
 PA (RAST/) RASTEBELT L.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (MEZE/) MEZES P S.
 PA (FURT/) FURTAK K.
 PA (PATR/) PATURAJAN M.
 PA (BURG/) BURGESS C E.

PA (MALY/) MALYANKAR U M.
 PA (SHIM/) SHIMKETS R A.
 PA (TAUP/) TAUPIER R J.
 PA (EDIN/) EDINGER S.
 PA (MAZU/) MAZUR A.
 Query Match
 Best Local Similarity 16.0%; Score 288.5; DB 8; Length 1953;
 RESULT 684
 ID ABB83136 standard; protein; 3645 AA.
 DE Human hemocytin protein - SEQ ID 127.
 PN US2003170630-A1.
 PD 11-SEP-2003.
 PA (ALSO/) ALSOBROOK J P.
 PA (TCHE/) TCHERNEV V T.
 PA (LIUX/) LIU X.
 PA (SPYT/) SPYTEK K A.
 PA (ZERR/) ZERHUSEN B D.
 PA (PATR/) PATURAJAN M.
 PA (LEPL/) LEPLLEY D M.
 PA (BURG/) BURGESS C E.
 PA (SHIM/) SHIMKETS R A.
 PA (GROS/) GROSSE W M.
 PA (SZEK/) SZEKERES E S.
 PA (VERN/) VERNET C A M.
 PA (LILU/) LI L.
 PA (CASW/) CASMAN S J.
 PA (BOLD/) BOLDOG F L.
 PA (GORM/) GORMAN L.
 PA (GANG/) GANGOLLI E A.
 PA (FERN/) FERNANDES E R.
 PA (RIEG/) RIEGER D K.
 PA (EDIN/) EDINGER S R.
 PA (GUNT/) GUNTHER E.
 PA (MILK/) MILLET I.
 PA (SCIO/) SCIORE P.
 PA (EILE/) EILERMAN K.
 PA (MACD/) MACDOUGALL J R.
 PA (SMIT/) SMITHSON G.
 Query Match
 Best Local Similarity 16.0%; Score 288.5; DB 7; Length 3645;
 RESULT 685
 ID ABB60991 standard; protein; 5635 AA.
 DE Novel human protein. SEQ ID 78.
 PN W0200250105-A1.
 PD 27-JUN-2002.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (GLAX) GLAXO GROUP LTD.
 Query Match
 Best Local Similarity 16.0%; Score 288.5; DB 5; Length 5635;
 RESULT 686
 ID ABB39841 standard; protein; 1708 AA.
 DE Protein similar to human NOV9 #2.
 PN US2003203843-A1.
 PD 30-OCT-2003.
 PA (PENNA) PENNA C E A.
 PA (GUOX/) GUO X.
 PA (SHIM/) SHIMKETS R A.
 PA (PADI/) PADIGARU M.
 PA (KEKU/) KEKUDA R.
 PA (SPYT/) SPYTEK K A.
 PA (MEHR/) MEHRABAN F.
 PA (TOPP/) TOPPER J N.
 PA (MALY/) MALYANKAR U M.
 PA (WASS/) WASSERMAN S M.
 PA (EDIN/) EDINGER S R.
 PA (SMIT/) SMITHSON G.
 PA (GUNT/) GUNTHER E.
 PA (KOMU/) KOMUVES L.
 Query Match
 Best Local Similarity 15.9%; Score 287.5; DB 7; Length 1708;
 RESULT 687
 ID ABB63044 standard; protein; 467 AA.

DE Drosophila melanogaster polypeptide SEQ ID NO 15924.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 15.8%; Score 284.5; DB 4; Length 467;
Best Local Similarity 26.1%; Pred. No. 1.1e-15;
RESULT 688
ID ADE63330 standard; protein; 858 AA.
DE Rat Protein P13596, SEQ ID NO 9268.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 15.4%; Score 277.5; DB 7; Length 858;
Best Local Similarity 25.5%; Pred. No. 1.1e-14;
RESULT 689
ID ADA55624 standard; protein; 733 AA.
DE Human protein, SEQ ID 3192.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 15.3%; Score 276; DB 6; Length 733;
Best Local Similarity 25.7%; Pred. No. 1.1e-14;
RESULT 690
ID ADE63332 standard; protein; 761 AA.
DE Human Protein P13592, SEQ ID NO 9270.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 15.3%; Score 276; DB 7; Length 761;
Best Local Similarity 25.7%; Pred. No. 1.2e-14;
RESULT 691
ID AAH8565 standard; protein; 848 AA.
DE Human NCAM 140KD Isoform precursor amino acid sequence.
PN WO2001018801-A2.
PD 06-APR-2000.
PA (RONN/) RONN L C B.
PA (BOCK/) BOCK E.
PA (HOLM/) HOLM A.
PA (OLSE/) OLSEN M.
PA (OSTE/) OSTERGAARD S.
PA (JENS/) JENSEN P H.
PA (POUL/) POULSEN F M.
PA (SORO/) SOROKA V.
PA (RALE/) RALETS I.
PA (BERE/) BEREZIN V.
Query Match 15.3%; Score 276; DB 3; Length 848;
Best Local Similarity 25.7%; Pred. No. 1.4e-14;
RESULT 692
ID AAH17222 standard; protein; 848 AA.
DE Human 140kd NCAM Isoform protein.
PN WO200196364-A2.
PD 20-DEC-2001.
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
PA (UNLO) KINGS COLLEGE LONDON.
Query Match 15.3%; Score 276; DB 5; Length 848;
Best Local Similarity 25.7%; Pred. No. 1.4e-14;
RESULT 693
ID AD124546 standard; protein; 848 AA.
DE Human modifier of Chk1 (MCHK) protein SEQ ID NO:96.
PN WO2004004785-A1.
PD 15-JAN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 15.3%; Score 276; DB 8; Length 848;
Best Local Similarity 25.7%; Pred. No. 1.4e-14;
RESULT 694
ID ADR28603 standard; protein; 853 AA.
DE Bovine NCAM-140 protein - SED ID 513.
PN WO2003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.

Query Match 15.3%; Score 275.5; DB 7; Length 853;
Best Local Similarity 25.5%; Pred. No. 1.6e-14;
RESULT 695
ID ADL36019 standard; protein; 90 AA.
DE Human NOVX-related polypeptide #17.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR V M.
PA (SHEN/) SHENY S G.
PA (SPYT/) SPYTEK R A.
PA (ZERR/) ZERRHUSEN B D.
PA (PART/) PARTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPITER R J.
PA (LILU/) LI L.
PA (PADI/) PADIGARU M.
Query Match 15.2%; Score 275; DB 7; Length 90;
Best Local Similarity 61.8%; Pred. No. 7.9e-16;
RESULT 696
ID AD25619 standard; protein; 848 AA.
DE Binding domain-immunoglobulin fusion protein-associated protein #87.
PN US2003118592-A1.
PD 26-JUN-2003.
PA (GENE-) GENE-CRAFT INC.
Query Match 15.2%; Score 275; DB 7; Length 848;
Best Local Similarity 25.7%; Pred. No. 1.7e-14;
RESULT 697
ID AAE37177 standard; protein; 1477 AA.
DE Human LRRCAPS protein #2.
PN WO2003035831-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 15.2%; Score 274; DB 6; Length 1477;
Best Local Similarity 29.2%; Pred. No. 4.4e-14;
RESULT 698
ID ADH48824 standard; protein; 1356 AA.
DE NOV45B protein sequence, SEQ ID 108.
PN WO200268652-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 15.1%; Score 273.5; DB 5; Length 1356;
Best Local Similarity 29.6%; Pred. No. 4.4e-14;
RESULT 699
ID ADH48822 standard; protein; 1426 AA.
DE NOV45A protein sequence, SEQ ID 106.
PN WO200268652-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 15.0%; Score 271.5; DB 5; Length 1426;
Best Local Similarity 29.6%; Pred. No. 6.9e-14;
RESULT 700
ID AAO30845 standard; protein; 859 AA.
DE Human cell adhesion and extracellular matrix protein (CADECM)-35.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.0%; Score 271; DB 7; Length 859;
Best Local Similarity 24.8%; Pred. No. 3.8e-14;
RESULT 701
ID ABB68566 standard; protein; 729 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 32490.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 15.0%; Score 270; DB 4; Length 729;
Best Local Similarity 26.7%; Pred. No. 3.7e-14;
RESULT 702
ID AAU18023 standard; protein; 152 AA.
DE Human Immunoglobulin polypeptide SEQ ID NO 168.
PN WO200155315-A2.

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.9%; Score 269; DB 4; Length 152;
Best Local Similarity 42.3%; Pred. No. 5.3e-15;
RESULT 703
ID ADB31647 standard; protein; 152 AA.
DE Human novel protein SEQ ID NO 168.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.9%; Score 269; DB 7; Length 152;
Best Local Similarity 42.3%; Pred. No. 5.3e-15;
RESULT 704
ID ADR66889 standard; protein; 1469 AA.
DE Human prostatic carcinoma derived DNA SEQ ID 187 #4.
PN W02004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 14.9%; Score 268.5; DB 8; Length 1469;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 705
ID ADR65991 standard; protein; 1469 AA.
DE Human prostatic carcinoma derived protein SEQ ID 187 #1.
PN W02004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 14.9%; Score 268.5; DB 8; Length 1469;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 706
ID ADJ5717 standard; protein; 1479 AA.
DE Human peroxidase-melanoma antigen-related protein.
PN W02004019893-A2.
PD 11-MAR-2004.
PA (RIGE-) RIGEL PHARM INC.
Query Match 14.9%; Score 268.5; DB 8; Length 1479;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 707
ID AAW81030 standard; protein; 1496 AA.
DE Melanoma associated antigen MG50.
PN W09855133-A1.
PD 10-DEC-1998.
PA (REGC-) UNIV CALIFORNIA.
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
Query Match 14.9%; Score 268.5; DB 2; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 708
ID AAY70469 standard; protein; 1496 AA.
DE Human p53 target molecule; PRG2 protein.
PN W0200012526-A1.
PD 09-MAR-2000.
PA (UYPR-) UNIV PRINCETON.
Query Match 14.9%; Score 268.5; DB 3; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 709
ID ABU03498 standard; protein; 1496 AA.
DE Angiogenesis-associated human protein sequence #43.
PN W0200279492-A2.
PD 10-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 14.9%; Score 268.5; DB 6; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 710
ID ADB89024 standard; protein; 1496 AA.
DE TAT264.
PN W02003057160-A2.

PD 17-JUL-2003.
PA (GETH-) GENENTECH INC.
Query Match 14.9%; Score 268.5; DB 7; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 711
ID ADP28706 standard; protein; 1496 AA.
DE Human peroxidase-like MG50 protein - SED ID 616.
PN W02003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match 14.9%; Score 268.5; DB 7; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 712
ID ADQ18902 standard; protein; 1496 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1721.
PN W02004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 14.9%; Score 268.5; DB 8; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 713
ID ADQ89920 standard; protein; 1496 AA.
DE Antagonist of cell cycle progression polypeptide #175.
PN W02004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 14.9%; Score 268.5; DB 8; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 714
ID ADQ89914 standard; protein; 1496 AA.
DE Antagonist of cell cycle progression polypeptide #172.
PN W02004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 14.9%; Score 268.5; DB 8; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 715
ID ADR66092 standard; protein; 1496 AA.
DE Human prostatic carcinoma derived protein SEQ ID 288 #1.
PN W02004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 14.9%; Score 268.5; DB 8; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 716
ID ADR66434 standard; protein; 1496 AA.
DE Human prostatic carcinoma derived protein SEQ ID 288 #2.
PN W02004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 14.9%; Score 268.5; DB 8; Length 1496;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 717
ID ABB11587 standard; peptide; 1498 AA.
DE Human peroxidase homologue, SEQ ID NO:1957.
PN W0200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.9%; Score 268.5; DB 4; Length 1498;
Best Local Similarity 28.8%; Pred. No. 1.3e-13;
RESULT 718
ID ABO00762 standard; protein; 1498 AA.
DE Polypeptide encoded by novel human contig #13.
PN W02003023013-A2.
PD 20-MAR-2003.

PA (HYSE-) HYSEQ INC.
Query Match 14.9%; Score 268.5; DB 6; Length 1498;
Best Local Similarity 28.8%; Pred. NO. 1.3e-13;
RESULT 719
ID AAG02771 standard; protein; 58 AA.
DE Human secreted protein, SEQ ID NO: 6852.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 14.8%; Score 267; DB 3; Length 58;
Best Local Similarity 86.2%; Pred. NO. 2.1e-15;
RESULT 720
ID ABB97902 standard; protein; 142 AA.
DE Human secretory polypeptide (SPTM) 154.
PN WO20020756-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 14.6%; Score 263; DB 5; Length 142;
Best Local Similarity 44.1%; Pred. NO. 1.6e-14;
RESULT 721
ID AAY13563 standard; protein; 1395 AA.
DE Drosophila Robo 1 polypeptide.
PN WO992563-A1.
PD 27-MAY-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 14.5%; Score 261; DB 2; Length 1395;
Best Local Similarity 26.1%; Pred. NO. 5.4e-13;
RESULT 722
ID AAY08401 standard; protein; 1395 AA.
DE Drosophila sp. ROBO1 protein.
PN WO9920764-A1.
PD 29-APR-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 14.5%; Score 261; DB 2; Length 1395;
Best Local Similarity 26.1%; Pred. NO. 5.4e-13;
RESULT 723
ID ADB85335 standard; protein; 1395 AA.
DE Fruitfly nerve cell growth modulator SLIT-1-associated sequence #1.
PN US2003170727-A1.
PD 11-SEP-2003.
PA (GOOD/) GOODMAN C S.
PA (KIDD/) KIDD T.
PA (BROS/) BROSE K.
PA (TESS/) TESSIER-LAVIGNE M.
Query Match 14.5%; Score 261; DB 7; Length 1395;
Best Local Similarity 26.1%; Pred. NO. 5.4e-13;
RESULT 724
ID ABB62052 standard; protein; 496 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12948.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.4%; Score 260.5; DB 4; Length 496;
Best Local Similarity 26.2%; Pred. NO. 1.5e-13;
RESULT 725
ID ABB68257 standard; protein; 1395 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 31563.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.4%; Score 260; DB 4; Length 1395;
Best Local Similarity 26.1%; Pred. NO. 6.6e-13;
RESULT 726
ID AAY5366 standard; protein; 4412 AA.
DE Sequence g1/1017427/emb/CNA62189 from an alignment with protein 608.
PN WO9960164-A1.
PD 25-NOV-1999.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 14.3%; Score 259; DB 3; Length 4412;
Best Local Similarity 29.6%; Pred. NO. 3.9e-12;
RESULT 727
ID ABB74786 standard; protein; 31267 AA.
DE Human RGS11 protein.

PN WO2002103355-A1.
PD 27-DEC-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 14.3%; Score 259; DB 6; Length 31267;
Best Local Similarity 29.6%; Pred. NO. 5.7e-11;
RESULT 728
ID ADQ89964 standard; protein; 34350 AA.
DE Antagonist of cell cycle progression polypeptide #197.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 14.3%; Score 259; DB 8; Length 34350;
Best Local Similarity 29.6%; Pred. NO. 6.4e-11;
RESULT 729
ID ADM74171 standard; protein; 381 AA.
DE Human NOV3A protein sequence SegID10.
PN WO2004015079-A2.
PD 19-FEB-2004.
PA (CURA-) CURAGEN CORP.
Query Match 14.3%; Score 258.5; DB 8; Length 381;
Best Local Similarity 27.4%; Pred. NO. 1.5e-13;
RESULT 730
ID ADM56387 standard; protein; 404 AA.
DE Human cell adhesion molecule NOV12.
PN US2003082554-A1.
PD 01-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 14.2%; Score 256.5; DB 7; Length 404;
Best Local Similarity 27.4%; Pred. NO. 2.4e-13;
RESULT 731
ID AAY33741 standard; protein; 444 AA.
DE Beta-secretase.
PN US5942400-A.
PD 24-AUG-1999.
PA (ELAN-) ELAN PHARM INC.
Query Match 14.2%; Score 256; DB 2; Length 444;
Best Local Similarity 26.7%; Pred. NO. 3.1e-13;
RESULT 732
ID AAB47251 standard; protein; 444 AA.
DE Beta-secretase.
PN US6221645-B1.
PD 24-APR-2001.
PA (ELAN-) ELAN PHARM INC.
Query Match 14.2%; Score 256; DB 4; Length 444;
Best Local Similarity 26.7%; Pred. NO. 3.1e-13;
RESULT 733
ID ABB63920 standard; protein; 359 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 18552.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.1%; Score 255; DB 4; Length 359;
Best Local Similarity 24.9%; Pred. NO. 2.8e-13;
RESULT 734
ID ADN24208 standard; protein; 5175 AA.
DE Bacterial polypeptide #6861.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.1%; Score 254.5; DB 8; Length 5175;
Best Local Similarity 29.3%; Pred. NO. 1.2e-11;
RESULT 735
ID ADN24206 standard; protein; 5175 AA.
DE Bacterial polypeptide #6859.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X. 14.1%; Score 254.5; DB 8; Length 5175;
PA (GOLD/) GOLDMAN B S. 29.3%; Pred. No. 1.2e-11;
Query Match
RESULT 736
ID ADN24207 standard; protein; 5198 AA.
DE Bacterial polypeptide #6860.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 14.1%; Score 254.5; DB 8; Length 5198;
Best Local Similarity 29.3%; Pred. No. 1.2e-11;
RESULT 737
ID ADN24205 standard; protein; 5198 AA.
DE Bacterial polypeptide #6858.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 14.1%; Score 254.5; DB 8; Length 5198;
Best Local Similarity 29.3%; Pred. No. 1.2e-11;
RESULT 738
ID ADM74177 standard; protein; 306 AA.
DE Human NOV3D protein sequence SegId16.
PN WO2004015079-A2.
PD 19-FEB-2004.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 14.0%; Score 253.5; DB 8; Length 306;
Best Local Similarity 27.1%; Pred. No. 3e-13;
RESULT 739
ID ABG66677 standard; protein; 404 AA.
DE Human novel polypeptide #12.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 14.0%; Score 253.5; DB 5; Length 404;
Best Local Similarity 27.1%; Pred. No. 4.4e-13;
RESULT 740
ID ABJ20221 standard; protein; 404 AA.
DE Human IG gene related protein SEQ ID No 44.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 14.0%; Score 253.5; DB 6; Length 404;
Best Local Similarity 27.1%; Pred. No. 4.4e-13;
RESULT 741
ID ADF66751 standard; protein; 404 AA.
DE Novel human protein NOV12.
PN US2003199103-A1.
PD 23-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 14.0%; Score 253.5; DB 8; Length 404;
Best Local Similarity 27.1%; Pred. No. 4.4e-13;
RESULT 742
ID ADI19788 standard; protein; 404 AA.
DE Human NOV12 protein.
PN US2004002134-A1.
PD 01-JAN-2004.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 14.0%; Score 253.5; DB 8; Length 404;
Best Local Similarity 27.1%; Pred. No. 4.4e-13;
RESULT 743
ID ADO60261 standard; protein; 404 AA.
DE Human NOV12 protein.
PN US2003134430-A1.
PD 17-JUL-2003.

PA (CURA-) CURAGEN CORP. 14.0%; Score 253.5; DB 8; Length 404;
Query Match
Best Local Similarity 27.1%; Pred. No. 4.4e-13;
RESULT 744
ID ADO47378 standard; protein; 568 AA.
DE Human neurotrophin-like protein-related protein SegId13.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match
Best Local Similarity 14.0%; Score 253; DB 8; Length 568;
Best Local Similarity 27.4%; Pred. No. 7.8e-13;
RESULT 745
ID ABB76023 standard; protein; 570 AA.
DE Neurotrophin-like polypeptide.
PN WO200157175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 14.0%; Score 253; DB 4; Length 570;
Best Local Similarity 27.4%; Pred. No. 7.8e-13;
RESULT 746
ID ABB76018 standard; protein; 586 AA.
DE Neurotrophin-like polypeptide splice variant.
PN WO200157175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 14.0%; Score 253; DB 4; Length 586;
Best Local Similarity 27.4%; Pred. No. 8.1e-13;
RESULT 747
ID ADO47372 standard; protein; 586 AA.
DE Human neurotrophin-like protein SegId7.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Query Match
Best Local Similarity 14.0%; Score 253; DB 8; Length 586;
Best Local Similarity 27.4%; Pred. No. 8.1e-13;
RESULT 748
ID ABO23244 standard; protein; 404 AA.
DE Human breast tumour associated protein 47-like polypeptide NOV12.
PN US2003027158-A1.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 13.9%; Score 251.5; DB 6; Length 404;
Best Local Similarity 27.1%; Pred. No. 6.6e-13;
RESULT 749
ID AAB61142 standard; protein; 404 AA.
DE Human NOV12 protein.
PN WO200075321-A2.
PD 14-DEC-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 13.9%; Score 250.5; DB 4; Length 404;
Best Local Similarity 27.1%; Pred. No. 8e-13;
RESULT 750
ID ABB61502 standard; protein; 885 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11298.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match
Best Local Similarity 13.9%; Score 250.5; DB 4; Length 885;
Best Local Similarity 26.5%; Pred. No. 2.3e-12;
RESULT 751
ID ABB76016 standard; protein; 374 AA.
DE Neurotrophin-like polypeptide.
PN WO200157175-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 13.8%; Score 250; DB 4; Length 374;
Best Local Similarity 27.7%; Pred. No. 8e-13;
RESULT 752
ID ADO47381 standard; protein; 374 AA.
DE Human neurotrophin-like protein-related protein SegId16.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.

Query Match 13.8%; Score 250; DB 8; Length 374;
 Best Local Similarity 27.7%; Pred. No. 8e-13;
 RESULT 753
 ID ADO47377 standard; protein; 440 AA.
 DE Human neurotrophin-like protein-related protein SegID12.
 PN WO2004039942-A2.
 PD 13-MAY-2004.
 PA (NUVE-) NUVELO.
 Query Match 13.8%; Score 250; DB 8; Length 440;
 Best Local Similarity 27.7%; Pred. No. 9.9e-13;
 RESULT 754
 ID ABB76022 standard; protein; 442 AA.
 DE Neurotrophin-like polypeptide.
 PN WO200157175-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 13.8%; Score 250; DB 4; Length 442;
 Best Local Similarity 27.7%; Pred. No. 1e-12;
 RESULT 755
 ID ABB76017 standard; protein; 458 AA.
 DE Neurotrophin-like polypeptide.
 PN WO200157175-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 13.8%; Score 250; DB 4; Length 458;
 Best Local Similarity 27.7%; Pred. No. 1e-12;
 RESULT 756
 ID ADO47369 standard; protein; 458 AA.
 DE Human neurotrophin-like protein SegID4.
 PN WO2004039942-A2.
 PD 13-MAY-2004.
 PA (NUVE-) NUVELO.
 Query Match 13.8%; Score 250; DB 8; Length 458;
 Best Local Similarity 27.7%; Pred. No. 1e-12;
 RESULT 757
 ID ADS10607 standard; protein; 458 AA.
 DE Human therapeutic protein - SEQ ID 844.
 PN WO2004080148-A2.
 PD 23-SEP-2004.
 PA (NUVE-) NUVELO INC.
 Query Match 13.8%; Score 250; DB 8; Length 458;
 Best Local Similarity 27.7%; Pred. No. 1e-12;
 RESULT 758
 ID ADO47385 standard; protein; 880 AA.
 DE Human neurotrophin-like protein-related protein SegID13.
 PN WO2004039942-A2.
 PD 13-MAY-2004.
 PA (NUVE-) NUVELO.
 Query Match 13.8%; Score 250; DB 8; Length 880;
 Best Local Similarity 27.7%; Pred. No. 2.6e-12;
 RESULT 759
 ID AAO30644 standard; protein; 886 AA.
 DE Human cell adhesion and extracellular matrix protein (CADECM)-34.
 PN WO2003047526-A2.
 PD 12-JUN-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 13.8%; Score 250; DB 7; Length 886;
 Best Local Similarity 27.7%; Pred. No. 2.6e-12;
 RESULT 760
 ID ADO47396 standard; protein; 955 AA.
 DE Human neurotrophin-like protein-related MAM domain GRIM protein SegID31.
 PN WO2004039942-A2.
 PD 13-MAY-2004.
 PA (NUVE-) NUVELO.
 Query Match 13.8%; Score 250; DB 8; Length 955;
 Best Local Similarity 27.7%; Pred. No. 2.9e-12;
 RESULT 761
 ID ADO47383 standard; protein; 955 AA.
 DE Human neurotrophin-like protein SegID8.
 PN WO2004039942-A2.
 PD 13-MAY-2004.
 PA (NUVE-) NUVELO.
 Query Match 13.8%; Score 250; DB 8; Length 955;

Best Local Similarity 27.7%; Pred. No. 2.9e-12;
 RESULT 762
 ID ADS10608 standard; protein; 955 AA.
 DE Human therapeutic protein - SEQ ID 845.
 PN WO2004080148-A2.
 PD 23-SEP-2004.
 PA (NUVE-) NUVELO INC.
 Query Match 13.8%; Score 250; DB 8; Length 955;
 Best Local Similarity 27.7%; Pred. No. 2.9e-12;
 RESULT 763
 ID ADS1107 standard; protein; 970 AA.
 DE Human therapeutic protein - SEQ ID 1344.
 PN WO2004080148-A2.
 PD 23-SEP-2004.
 PA (NUVE-) NUVELO INC.
 Query Match 13.8%; Score 250; DB 8; Length 970;
 Best Local Similarity 27.7%; Pred. No. 2.9e-12;
 RESULT 764
 ID ABG12100 standard; protein; 1219 AA.
 DE Novel human diagnostic protein #12091.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 13.8%; Score 250; DB 4; Length 1219;
 Best Local Similarity 27.7%; Pred. No. 4e-12;
 RESULT 765
 ID ABUS2336 standard; protein; 1315 AA.
 DE Human GPCR related protein NOV13a.
 PN WO200279398-A2.
 PD 10-OCT-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 13.8%; Score 250; DB 6; Length 1315;
 Best Local Similarity 27.7%; Pred. No. 4.4e-12;
 RESULT 766
 ID ADH72138 standard; protein; 1315 AA.
 DE Human protein of the invention NOV46h SEQ ID NO:1034.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 13.8%; Score 250; DB 8; Length 1315;
 Best Local Similarity 27.7%; Pred. No. 4.4e-12;
 RESULT 767
 ID ADL24007 standard; protein; 1315 AA.
 DE Human NOVX polypeptide #26.
 PN US2004002120-A1.
 PD 01-JAN-2004.
 PA (KEKU/) KEKUDA R.
 PA (TCHE/) TCHERNEV V. T.
 PA (LIXU/) LIU X.
 PA (SPYT/) SPYTEK K. A.
 PA (PATR/) PATTRAJAN M.
 PA (BURG/) BURGESS C. E.
 PA (VERN/) VERNET C. A. M.
 PA (LITL/) LI L.
 PA (GORM/) GORMAN L.
 PA (MALY/) MALYANKAR U. M.
 PA (BOLD/) BOLDIG F. L.
 PA (GUOX/) GUO X.
 PA (SHEN/) SHENOY S. G.
 PA (PADI/) PADIGARU M.
 PA (TAUP/) TAUPIER R. J.
 PA (MILL/) MILLER C. E.
 PA (CASW/) CASMAN S. J.
 PA (PENA/) PENA C. B. A.
 PA (GANG/) GANGOLI B. A.
 PA (GUSE/) GUSEV V. Y.
 PA (SMIT/) SMITHSON G.
 PA (ZERR/) ZERRHUSEN B. D.
 PA (GERL/) GERLACH V.
 PA (POCH/) POCHART P. F.
 PA (FERN/) FERNANDES E. R.
 PA (SHIM/) SHIMKETS R. A.
 PA (RAST/) RASTELLI L.

PA (SPAD/) SPADERNA S K.
PA (LARO/) LAROCHELLE W J.
PA (ZHON/) ZHONG M.
PA (KHRA/) KHRAMTSOV N V.
PA (VOSS/) VOSS E Z.
PA (HERR/) HERRMANN J L.
Query Match 13.8%; Score 250; DB 8; Length 1315;
Best Local Similarity 27.7%; Pred. No. 4.4e-12;
RESULT 768
ID ADH72134 standard; protein; 1335 AA.
DE Human protein of the invention NOV46f SEQ ID NO:1030.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 13.8%; Score 250; DB 8; Length 1335;
Best Local Similarity 27.7%; Pred. No. 4.5e-12;
RESULT 769
ID ABU52329 standard; protein; 1386 AA.
DE Human GPCR related protein NOV12a.
PN WO200279398-A2.
PD 10-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 13.8%; Score 250; DB 6; Length 1386;
Best Local Similarity 27.7%; Pred. No. 4.8e-12;
RESULT 770
ID ADL23993 standard; protein; 1386 AA.
DE Human NOVX polypeptide #19.
PN US2004002120-A1.
PD 01-JAN-2004.
PA (KEKU/) TCHERNY V T.
PA (TCHN/) TCHERNY V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (PATR/) PATURAJAN M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDGO F L.
PA (GUOX/) GUO X.
PA (SHEN/) SHENY S G.
PA (PADU/) PADIGARU M.
PA (TAUP/) TAUPIER R J.
PA (MILL/) MILLER C E.
PA (CASM/) CASMAN S J.
PA (PENA/) PENA C B A.
PA (GANG/) GANGOLI E A.
PA (GUSE/) GUSEV V Y.
PA (SMIT/) SMITHSON G.
PA (ZERN/) ZERHUSEN B D.
PA (GERL/) GERLACH V.
PA (POCH/) POCHART P F.
PA (PERN/) FERNANDES E R.
PA (SHIM/) SHIMKETS R A.
PA (RAST/) RASTELLI L.
PA (SPAD/) SPADERNA S K.
PA (LARO/) LAROCHELLE W J.
PA (ZHON/) ZHONG M.
PA (KHRA/) KHRAMTSOV N V.
PA (VOSS/) VOSS E Z.
PA (HERR/) HERRMANN J L.
Query Match 13.8%; Score 250; DB 8; Length 1386;
Best Local Similarity 27.7%; Pred. No. 4.8e-12;
RESULT 771
ID ADD47172 standard; protein; 1040 AA.
DE Human Protein NP_005067, SEQ ID NO 12866.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO/) GEN HOSPITAL CORP.
PA (FARB/) BAYER AG.
Query Match 13.8%; Score 249.5; DB 7; Length 1040;
Best Local Similarity 26.1%; Pred. No. 3.6e-12;

RESULT 772
ID ADO28581 standard; protein; 1040 AA.
DE Human axonin-1 precursor (AXO1) protein SEQ ID NO:10.
PN WO2004044178-A2.
PD 27-MAY-2004.
PA (GETH/) GENENTECH INC.
Query Match 13.8%; Score 249.5; DB 8; Length 1040;
Best Local Similarity 26.1%; Pred. No. 3.6e-12;
RESULT 773
ID ABO84729 standard; protein; 1040 AA.
DE Human cancer-associated protein HP22-025.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 13.8%; Score 249.5; DB 8; Length 1040;
Best Local Similarity 26.1%; Pred. No. 3.6e-12;
RESULT 774
ID ABO84728 standard; protein; 1040 AA.
DE Human cancer-associated protein HP22-025.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 13.8%; Score 249.5; DB 8; Length 1040;
Best Local Similarity 26.1%; Pred. No. 3.6e-12;
RESULT 775
ID ABB6882 standard; protein; 467 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 33438.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE/) PE CORP NY.
Query Match 13.7%; Score 248; DB 4; Length 467;
Best Local Similarity 27.4%; Pred. No. 1.6e-12;
RESULT 776
ID ADJ68312 standard; protein; 1007 AA.
DE Human heat mitochondrial protein as a therapeutic target Segid118.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 13.6%; Score 246.5; DB 7; Length 1007;
Best Local Similarity 24.6%; Pred. No. 6.2e-12;
RESULT 777
ID AAR63759 standard; protein; 1018 AA.
DE Human contactin (EMBL Accession #Z21488).
PN EP618293-A1.
PD 05-OCT-1994.
PA (BECT) BECTON DICKINSON CO.
Query Match 13.6%; Score 246.5; DB 2; Length 1018;
Best Local Similarity 24.6%; Pred. No. 6.3e-12;
RESULT 778
ID AAR87028 standard; protein; 1018 AA.
DE Human contactin.
PN WO9535373-A2.
PD 28-DEC-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 13.6%; Score 246.5; DB 2; Length 1018;
Best Local Similarity 24.6%; Pred. No. 6.3e-12;
RESULT 779
ID ADE71113 standard; protein; 1018 AA.
DE Contactin, SEQ ID 67.
PN WO2003070889-A2.
PD 28-AUG-2003.
PA (IDEC-) IDEC PHARM CORP.
Query Match 13.6%; Score 246.5; DB 7; Length 1018;
Best Local Similarity 24.6%; Pred. No. 6.3e-12;
RESULT 780
ID ADU73696 standard; protein; 1018 AA.
DE Marker gene related amino acid sequence SEQ ID NO:948.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 13.6%; Score 246.5; DB 8; Length 1018;
Best Local Similarity 24.6%; Pred. No. 6.3e-12;

RESULT 781
 ID ADO28659 standard; protein; 1018 AA.
 DE Human CONT protein SEQ ID NO:88.
 PN WO2004044178-A2.
 PD 27-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 13.6%; Score 246.5; DB 8; Length 1018;
 Best Local Similarity 24.6%; Pred. No. 6.3e-12;
 RESULT 782
 ID ADP67246 standard; protein; 1018 AA.
 DE Human P3/contactin protein.
 PN WO2004052389-A2.
 PD 24-JUN-2004.
 PA (SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.
 PA (FORR/) FORREST G R.
 Query Match 13.6%; Score 246.5; DB 8; Length 1018;
 Best Local Similarity 24.6%; Pred. No. 6.3e-12;
 RESULT 783
 ID ADR66068 standard; protein; 1073 AA.
 DE Human prostatic carcinoma derived protein SEQ ID 264 #1.
 PN WO2004076614-A2.
 PD 10-SEP-2004.
 PA (HINZ/) HINZMANN B.
 PA (DAHL/) DAHL E.
 PA (ROSE/) ROSENTHAL A.
 PA (HERM/) HERMANN K.
 PA (PLA/) PILARSKY C.
 Query Match 13.6%; Score 245.5; DB 8; Length 1073;
 Best Local Similarity 26.4%; Pred. No. 8.2e-12;
 RESULT 784
 ID ADR66410 standard; protein; 1073 AA.
 DE Human prostatic carcinoma derived protein SEQ ID 264 #2.
 PN WO2004076614-A2.
 PD 10-SEP-2004.
 PA (HINZ/) HINZMANN B.
 PA (DAHL/) DAHL E.
 PA (ROSE/) ROSENTHAL A.
 PA (HERM/) HERMANN K.
 PA (PLA/) PILARSKY C.
 Query Match 13.6%; Score 245.5; DB 8; Length 1073;
 Best Local Similarity 26.4%; Pred. No. 8.2e-12;
 RESULT 785
 ID ADA54925 standard; protein; 512 AA.
 DE Human protein, SEQ ID 2493.
 PN EP1293569-A2.
 PD 19-MAR-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 13.5%; Score 244.5; DB 6; Length 512;
 Best Local Similarity 27.8%; Pred. No. 3.6e-12;
 RESULT 786
 ID AAM06485 standard; peptide; 1018 AA.
 DE Rat contactin ligand for RPTbeta.
 PN WO9637776-A1.
 PD 28-NOV-1996.
 PA (SUGE-) SUGEN INC.
 Query Match 13.5%; Score 243.5; DB 2; Length 1018;
 Best Local Similarity 24.0%; Pred. No. 1.1e-11;
 RESULT 787
 ID ADE56173 standard; protein; 1021 AA.
 DE Rat protein Q63198, SEQ ID NO 2022.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GCHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 13.5%; Score 243.5; DB 7; Length 1021;
 Best Local Similarity 24.0%; Pred. No. 1.1e-11;
 RESULT 788
 ID ABG03059 standard; protein; 792 AA.
 DE Novel human diagnostic protein #3050.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.

Query Match 13.4%; Score 242.5; DB 4; Length 792;
 Best Local Similarity 26.4%; Pred. No. 9.8e-12;
 RESULT 789
 ID ABG00258 standard; protein; 893 AA.
 DE Novel human diagnostic protein #249.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 13.4%; Score 242.5; DB 4; Length 893;
 Best Local Similarity 26.4%; Pred. No. 1.2e-11;
 RESULT 790
 ID ABG00611 standard; protein; 893 AA.
 DE Novel human diagnostic protein #602.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 13.4%; Score 242.5; DB 4; Length 893;
 Best Local Similarity 26.4%; Pred. No. 1.2e-11;
 RESULT 791
 ID ABG31317 standard; protein; 2586 AA.
 DE Human 5+3 corrected OCP protein.
 PN WO200246364-A2.
 PD 13-JUN-2002.
 PA (QUAR-) QUARK BIOTECH INC.
 Query Match 13.4%; Score 242; DB 5; Length 2586;
 Best Local Similarity 27.0%; Pred. No. 5.5e-11;
 RESULT 792
 ID ABG32891 standard; protein; 2586 AA.
 DE Human osteoclast protein (OCP) #1.
 PN US2002086825-A1.
 PD 04-JUL-2002.
 PA (EINA/) EINAT P.
 PA (SEGE/) SEGEV O.
 PA (SKAL/) SKALITER R.
 PA (FEIN/) FEINSTEIN E.
 PA (FAER/) FAERMAN A.
 Query Match 13.4%; Score 242; DB 5; Length 2586;
 Best Local Similarity 27.0%; Pred. No. 5.5e-11;
 RESULT 793
 ID ADL02231 standard; protein; 2586 AA.
 DE Human OCP protein #1.
 PN US2004053301-A1.
 PD 18-MAR-2004.
 PA (QUAR-) QUARK BIOTECH INC.
 Query Match 13.4%; Score 242; DB 8; Length 2586;
 Best Local Similarity 27.0%; Pred. No. 5.5e-11;
 RESULT 794
 ID ADL02234 standard; protein; 2586 AA.
 DE Human OCP protein #2.
 PN US2004053301-A1.
 PD 18-MAR-2004.
 PA (QUAR-) QUARK BIOTECH INC.
 Query Match 13.4%; Score 242; DB 8; Length 2586;
 Best Local Similarity 27.0%; Pred. No. 5.5e-11;
 RESULT 795
 ID AAB47935 standard; protein; 2587 AA.
 DE Human OCP.
 PN US2002022026-A1.
 PD 21-FEB-2002.
 PA (EINA/) EINAT P.
 PA (SEGE/) SEGEV O.
 PA (SKAL/) SKALITER R.
 PA (FEIN/) FEINSTEIN E.
 PA (FAER/) FAERMAN A.
 Query Match 13.4%; Score 242; DB 5; Length 2587;
 Best Local Similarity 27.0%; Pred. No. 5.5e-11;
 RESULT 796
 ID ABG32896 standard; protein; 2587 AA.
 DE Human osteoclast protein (OCP) #2.
 PN US2002086825-A1.
 PD 04-JUL-2002.
 PA (EINA/) EINAT P.
 PA (SEGE/) SEGEV O.

PA (SKAL/) SKALITER R.
 PA (FEIN/) FEINSTEIN E.
 PA (FAER/) FAERMAN A.
 Query Match
 Best Local Similarity 13.4%; Score 242; DB 5; Length 2587;
 RESULT 797
 ID ADL02236 standard; protein; 2587 AA.
 DE Human OCP protein #3.
 PN US200405301-A1.
 PD 18-MAR-2004.
 PA (QUAR-) QUARK BIOTECH INC.
 Query Match
 Best Local Similarity 13.4%; Score 242; DB 8; Length 2587;
 RESULT 798
 ID ABG31323 standard; protein; 2589 AA.
 DE Human OCP protein.
 PN WO200246364-A2.
 PD 13-JUN-2002.
 PA (QUAR-) QUARK BIOTECH INC.
 Query Match
 Best Local Similarity 13.4%; Score 242; DB 5; Length 2589;
 RESULT 799
 ID ADL02244 standard; protein; 2589 AA.
 DE Human OCP protein #5.
 PN US200405301-A1.
 PD 18-MAR-2004.
 PA (QUAR-) QUARK BIOTECH INC.
 Query Match
 Best Local Similarity 13.4%; Score 242; DB 8; Length 2589;
 RESULT 800
 ID AAR92256 standard; protein; 582 AA.
 DE Neural cell adhesion molecule splice variant.
 PN WO9604396-A1.
 PD 15-FEB-1996.
 PA (SYST-) SYSTEMIX INC.
 Query Match
 Best Local Similarity 13.4%; Score 241.5; DB 2; Length 582;
 RESULT 801
 ID AAR92255 standard; protein; 761 AA.
 DE Neural cell adhesion molecule.
 PN WO9604396-A1.
 PD 15-FEB-1996.
 PA (SYST-) SYSTEMIX INC.
 Query Match
 Best Local Similarity 13.4%; Score 241.5; DB 2; Length 761;
 RESULT 802
 ID ADI24547 standard; protein; 837 AA.
 DE Human modifier of Chk1 (MCHK) protein SEQ ID NO:97.
 PN WO2004004785-A1.
 PD 15-JAN-2004.
 PA (EXEL-) EXELIXIS INC.
 Query Match
 Best Local Similarity 13.4%; Score 241.5; DB 8; Length 837;
 RESULT 803
 ID ADU76385 standard; protein; 1020 AA.
 DE Marker gene related amino acid sequence SEQ ID NO:1637.
 PN EP1394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INC.
 Query Match
 Best Local Similarity 13.4%; Score 241.5; DB 8; Length 1020;
 RESULT 804
 ID ABG07536 standard; protein; 891 AA.
 DE Novel human diagnostic protein #7527.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 13.3%; Score 241; DB 4; Length 891;
 RESULT 805
 ID ABP69251 standard; protein; 2173 AA.
 DE Human polypeptide SEQ ID NO 1298.
 PN WO200270539-A2.

PD 12-SEP-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 13.3%; Score 241; DB 5; Length 2173;
 RESULT 806
 ID AAE00585 standard; protein; 793 AA.
 DE Human nuclear cell adhesion molecule homologue, NCAM_c_1 protein.
 PN WO200129215-A2.
 PD 26-APR-2001.
 PA (COMP-) COMPUGEN LTD.
 Query Match
 Best Local Similarity 13.2%; Score 238.5; DB 4; Length 793;
 RESULT 807
 ID AAE00584 standard; protein; 848 AA.
 DE Human nuclear cell adhesion molecule homologue, NCAM_c_2 protein.
 PN WO200129215-A2.
 PD 26-APR-2001.
 PA (COMP-) COMPUGEN LTD.
 Query Match
 Best Local Similarity 13.2%; Score 238.5; DB 4; Length 848;
 RESULT 808
 ID AAE00586 standard; protein; 891 AA.
 DE Human nuclear cell adhesion molecule homologue, NCAM_d_2 protein.
 PN WO200129215-A2.
 PD 26-APR-2001.
 PA (COMP-) COMPUGEN LTD.
 Query Match
 Best Local Similarity 13.2%; Score 238.5; DB 4; Length 891;
 RESULT 809
 ID AAE00583 standard; protein; 920 AA.
 DE Human cell adhesion molecule homologue (CAM-H) protein #2.
 PN WO200129215-A2.
 PD 26-APR-2001.
 PA (COMP-) COMPUGEN LTD.
 Query Match
 Best Local Similarity 13.2%; Score 238.5; DB 4; Length 920;
 RESULT 810
 ID AAE00582 standard; protein; 946 AA.
 DE Human nuclear cell adhesion molecule homologue, NCAM_d_1 protein.
 PN WO200129215-A2.
 PD 26-APR-2001.
 PA (COMP-) COMPUGEN LTD.
 Query Match
 Best Local Similarity 13.2%; Score 238.5; DB 4; Length 946;
 RESULT 811
 ID AAE00581 standard; protein; 1018 AA.
 DE Human cell adhesion molecule homologue (CAM-H) protein #1.
 PN WO200129215-A2.
 PD 26-APR-2001.
 PA (COMP-) COMPUGEN LTD.
 Query Match
 Best Local Similarity 13.2%; Score 238.5; DB 4; Length 1018;
 RESULT 812
 ID AAM05161 standard; protein; 73 AA.
 DE Human LAMP residues 46-118.
 PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDNJ-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Query Match
 Best Local Similarity 13.1%; Score 237; DB 2; Length 73;
 RESULT 813
 ID AAM05162 standard; protein; 73 AA.
 DE Rat LAMP residues 46-118.
 PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDNJ-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Query Match
 Best Local Similarity 13.1%; Score 237; DB 2; Length 73;
 RESULT 814
 ID ADR09877 standard; protein; 632 AA.
 DE Human protein useful for treating neurological disease Seq 3383.
 PN EP1447413-A2.
 PD 18-AUG-2004.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 13.0%; Score 235.5; DB 8; Length 632;
Best Local Similarity 26.9%; Pred. No. 2.9e-11;
RESULT 815
ID ADH71818 standard; protein; 967 AA.
DE Human protein of the invention NOV29y SEQ ID NO:714.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 13.0%; Score 235.5; DB 8; Length 967;
Best Local Similarity 27.1%; Pred. No. 5.2e-11;
RESULT 816
ID ADS10576 standard; protein; 2428 AA.
DE Human therapeutic protein - SEQ ID 813.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NOVE-) NOVELO INC.
Query Match 13.0%; Score 235.5; DB 8; Length 2428;
Best Local Similarity 26.9%; Pred. No. 1.8e-10;
RESULT 817
ID ADL02252 standard; protein; 2623 AA.
DE Human OCP protein #7.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 13.0%; Score 235.5; DB 8; Length 2623;
Best Local Similarity 26.9%; Pred. No. 2e-10;
RESULT 818
ID ADS10577 standard; protein; 2623 AA.
DE Human therapeutic protein - SEQ ID 814.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NOVE-) NOVELO INC.
Query Match 13.0%; Score 235.5; DB 8; Length 2623;
Best Local Similarity 26.9%; Pred. No. 2e-10;
RESULT 819
ID ADN24073 standard; protein; 662 AA.
DE Bacterial polypeptide #6726.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 13.0%; Score 235.5; DB 8; Length 662;
Best Local Similarity 25.5%; Pred. No. 3.4e-11;
RESULT 820
ID ADD47171 standard; protein; 1040 AA.
DE Rat protein AAA42201, SEQ ID NO 12864.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (PARB) BAYER AG.
Query Match 13.0%; Score 234.5; DB 7; Length 1040;
Best Local Similarity 25.8%; Pred. No. 7e-11;
RESULT 821
ID ADRE7266 standard; protein; 1100 AA.
DE Human bladder cancer associated amino acid sequence.
PN WO2004076613-A2.
PD 10-SEP-2004.
PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUD E.
PA (PLA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Query Match 12.9%; Score 233.5; DB 8; Length 1100;
Best Local Similarity 24.9%; Pred. No. 9.2e-11;
RESULT 822
ID ADH71816 standard; protein; 967 AA.
DE Human protein of the invention NOV29x SEQ ID NO:712.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2591;
Best Local Similarity 26.9%; Pred. No. 4e-10;
RESULT 823
ID ADN23691 standard; protein; 2783 AA.
DE Bacterial polypeptide #6344.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.9%; Score 232.5; DB 8; Length 2783;
Best Local Similarity 23.5%; Pred. No. 4e-10;
RESULT 824
ID ABG69614 standard; protein; 2401 AA.
DE Human NOV12a protein.
PN WO200250277-A2.
PD 27-JUN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 5; Length 2401;
Best Local Similarity 26.9%; Pred. No. 3.6e-10;
RESULT 825
ID ABG69619 standard; protein; 2447 AA.
DE Human NOV12f protein.
PN WO200250277-A2.
PD 27-JUN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 5; Length 2447;
Best Local Similarity 26.9%; Pred. No. 3.7e-10;
RESULT 826
ID ADH83065 standard; protein; 2591 AA.
DE Human NOVX NOV12f protein.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOOROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LITX/) LIU X.
PA (SPYX/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATY/) PATYURAJAN M.
PA (LEPL/) LEPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LITL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (PERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MITL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 12.8%; Score 232; DB 7; Length 2591;
Best Local Similarity 26.9%; Pred. No. 4e-10;
RESULT 827
ID ADH71822 standard; protein; 2591 AA.
DE Human protein of the invention NOV29aa SEQ ID NO:718.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2591;
Best Local Similarity 26.9%; Pred. No. 4e-10;

RESULT 828
ID ADH71820 standard; protein; 2602 AA.
DE Human protein of the invention NOV29z SEQ ID NO:716.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2602;
Best Local Similarity 26.9%; Pred. No. 4e-10;
RESULT 829
ID ADH83055 standard; protein; 2617 AA.
DE Human NOVX NOV12a protein.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (LEPL/) LEPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 12.8%; Score 232; DB 7; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 830
ID ADH71842 standard; protein; 2617 AA.
DE Human protein of the invention NOV29ak SEQ ID NO:738.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 831
ID ADH71852 standard; protein; 2617 AA.
DE Human protein of the invention NOV29ap SEQ ID NO:748.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 832
ID ADH71838 standard; protein; 2617 AA.
DE Human protein of the invention NOV29ai SEQ ID NO:734.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 833
ID ADH71770 standard; protein; 2617 AA.
DE Human protein of the invention NOV29a SEQ ID NO:666.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;

RESULT 834
ID ADH71836 standard; protein; 2617 AA.
DE Human protein of the invention NOV29ah SEQ ID NO:732.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 835
ID ADH71840 standard; protein; 2617 AA.
DE Human protein of the invention NOV29aj SEQ ID NO:736.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 836
ID ADH71844 standard; protein; 2617 AA.
DE Human protein of the invention NOV29al SEQ ID NO:740.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 837
ID ADH71846 standard; protein; 2617 AA.
DE Human protein of the invention NOV29am SEQ ID NO:742.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 838
ID ADH71850 standard; protein; 2617 AA.
DE Human protein of the invention NOV29ao SEQ ID NO:746.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 839
ID ADH71854 standard; protein; 2617 AA.
DE Human protein of the invention NOV29aq SEQ ID NO:750.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 840
ID ADH71848 standard; protein; 2617 AA.
DE Human protein of the invention NOV29an SEQ ID NO:744.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 841
ID ABU07377 standard; protein; 3931 AA.
DE Human protein NOV9.
PN W0200285922-A2.
PD 31-OCT-2002.
PA (MILL-) MILLENNIUM PHARM INC.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 6; Length 3931;
Best Local Similarity 28.3%; Pred. No. 7.1e-10;
RESULT 842
ID AAW29667 standard; protein; 1028 AA.
DE Homo sapiens DL185_1 clone secreted protein.
PN W09830695-A2.
PD 16-JUL-1998.
PA (GEMY) GENETICS INST INC.
Query Match 12.8%; Score 231; DB 2; Length 1028;
Best Local Similarity 26.7%; Pred. No. 1.4e-10;

RESULT 843
ID ADP67247 standard; protein; 1028 AA.
DE Human NB-3 protein.
PN WO2004052389-A2.
PD 24-JUN-2004.
PA (SAGE-) SINGAPORE GEN HOSPITAL PTE LTD.
PA (FORR/) FORREST G R.
Query Match
Best Local Similarity 12.8%; Score 231; DB 8; Length 1028;
Best Local Similarity 26.7%; Pred. No. 1.4e-10;
RESULT 844
ID ADG39786 standard; protein; 3931 AA.
DE Human novel protein NOV9.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENNA/) PENNA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
Query Match
Best Local Similarity 12.8%; Score 231; DB 7; Length 3931;
Best Local Similarity 28.3%; Pred. No. 8.6e-10;
RESULT 845
ID AAW26507 standard; protein; 868 AA.
DE Rat Dmk receptor.
PN US656473-A.
PD 12-AUG-1997.
PA (REG-) REGENERON PHARM INC.
Query Match
Best Local Similarity 12.8%; Score 230.5; DB 2; Length 868;
Best Local Similarity 25.2%; Pred. No. 1.2e-10;
RESULT 846
ID AAW26610 standard; protein; 868 AA.
DE Rat muscle-specific kinase (Musk).
PN WO9721811-A2.
PD 19-JUN-1997.
PA (REG-) REGENERON PHARM INC.
Query Match
Best Local Similarity 12.8%; Score 230.5; DB 2; Length 868;
Best Local Similarity 25.2%; Pred. No. 1.2e-10;
RESULT 847
ID ADH71830 standard; protein; 961 AA.
DE Human protein of the invention NOV29ae SEQ ID NO:726.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 12.8%; Score 230.5; DB 8; Length 961;
Best Local Similarity 27.2%; Pred. No. 1.4e-10;
RESULT 848
ID ADH71832 standard; protein; 961 AA.
DE Human protein of the invention NOV29af SEQ ID NO:728.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 12.8%; Score 230.5; DB 8; Length 961;
Best Local Similarity 27.2%; Pred. No. 1.4e-10;
RESULT 849
ID ABO84727 standard; protein; 1040 AA.
DE Mouse cancer-associated protein MP22-025.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 12.8%; Score 230.5; DB 8; Length 1040;
Best Local Similarity 25.0%; Pred. No. 1.5e-10;
RESULT 850
ID ABO84469 standard; protein; 3475 AA.
DE Human cancer-associated protein HP13-036.1.

PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 12.8%; Score 230.5; DB 8; Length 3475;
Best Local Similarity 24.3%; Pred. No. 8.1e-10;
RESULT 851
ID ADG39842 standard; protein; 1928 AA.
DE Protein similar to human NOV9 #3.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENNA/) PENNA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
Query Match
Best Local Similarity 12.7%; Score 230; DB 7; Length 1928;
Best Local Similarity 22.9%; Pred. No. 4e-10;
RESULT 852
ID ADG39843 standard; protein; 1951 AA.
DE Protein similar to human NOV9 #4.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENNA/) PENNA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
Query Match
Best Local Similarity 12.7%; Score 230; DB 7; Length 1951;
Best Local Similarity 22.9%; Pred. No. 4e-10;
RESULT 853
ID AAY53667 standard; protein; 3117 AA.
DE Sequence gi/3328186 from an alignment with protein 608.
PN WO960164-A1.
PD 25-NOV-1999.
PA (QUAR-) QUARK BIOTECH INC.
Query Match
Best Local Similarity 12.7%; Score 230; DB 3; Length 3117;
Best Local Similarity 22.9%; Pred. No. 7.7e-10;
RESULT 854
ID AAB31089 standard; protein; 4393 AA.
DE Amino acid sequence of a human protein.
PN WO200105422-A2.
PD 25-JAN-2001.
PA (INMR-) BIOMERIEUX STELHVS.
Query Match
Best Local Similarity 12.7%; Score 230; DB 4; Length 4393;
Best Local Similarity 26.0%; Pred. No. 1.2e-09;
RESULT 855
ID ADJ35758 standard; protein; 4393 AA.
DE Human perlecan (heparan sulphate proteoglycan 2; HSPG2) protein.
PN WO2004019893-A2.
PD 11-MAR-2004.
PA (RIGE-) RIGEL PHARM INC.
Query Match
Best Local Similarity 12.7%; Score 230; DB 8; Length 4393;
Best Local Similarity 26.0%; Pred. No. 1.2e-09;
RESULT 856
ID ADG39442 standard; protein; 4393 AA.

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1105.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLEERA CORP.
Query Match 12.7%; Score 230; DB 8; Length 4393;
Best Local Similarity 26.0%; Pred. No. 1.2e-09;
RESULT 857
ID ABG23265 standard; protein; 4436 AA.
DE Novel human diagnostic protein #23256.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.7%; Score 230; DB 4; Length 4436;
Best Local Similarity 26.0%; Pred. No. 1.2e-09;
RESULT 858
ID ADL16585 standard; protein; 849 AA.
DE Human 282P1G3 polypeptide #35.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 849;
Best Local Similarity 25.6%; Pred. No. 1.4e-10;
RESULT 859
ID ADL16586 standard; protein; 851 AA.
DE Human 282P1G3 polypeptide #36.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 851;
Best Local Similarity 25.6%; Pred. No. 1.4e-10;
RESULT 860
ID AAM26506 standard; protein; 869 AA.
DE Human Dmk receptor.
PN US5656473-A.
PD 12-AUG-1997.
PA (REG-) REGENERON PHARM INC.
Query Match 12.7%; Score 229.5; DB 2; Length 869;
Best Local Similarity 26.4%; Pred. No. 1.5e-10;
RESULT 861
ID AAM26611 standard; protein; 869 AA.
DE Human muscle-specific kinase (MUSK).
PN WO9721811-A2.
PD 19-JUN-1997.
PA (REG-) REGENERON PHARM INC.
Query Match 12.7%; Score 229.5; DB 2; Length 869;
Best Local Similarity 26.4%; Pred. No. 1.5e-10;
RESULT 862
ID ADO08944 standard; protein; 869 AA.
DE Antagonist of cell cycle progression polypeptide #137.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 12.7%; Score 229.5; DB 8; Length 869;
Best Local Similarity 26.4%; Pred. No. 1.5e-10;
RESULT 863
ID ADL16446 standard; protein; 893 AA.
DE Human 282P1G3 polypeptide #12.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 893;
Best Local Similarity 25.6%; Pred. No. 1.5e-10;
RESULT 864
ID ADL16584 standard; protein; 893 AA.
DE Human 282P1G3 polypeptide #34.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 893;
Best Local Similarity 25.6%; Pred. No. 1.5e-10;
RESULT 865
ID ADL16625 standard; protein; 893 AA.
DE Human 282P1G3 polypeptide #57.

PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 893;
Best Local Similarity 25.6%; Pred. No. 1.5e-10;
RESULT 866
ID ADL16431 standard; protein; 893 AA.
DE Human 282P1G3 polypeptide #3.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 893;
Best Local Similarity 25.6%; Pred. No. 1.5e-10;
RESULT 867
ID ADL16626 standard; protein; 1117 AA.
DE Human 282P1G3 polypeptide #58.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1117;
Best Local Similarity 25.6%; Pred. No. 2.1e-10;
RESULT 868
ID ADL16590 standard; protein; 1117 AA.
DE Human 282P1G3 polypeptide #37.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1117;
Best Local Similarity 25.6%; Pred. No. 2.1e-10;
RESULT 869
ID ADL16447 standard; protein; 1117 AA.
DE Human 282P1G3 polypeptide #13.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1117;
Best Local Similarity 25.6%; Pred. No. 2.1e-10;
RESULT 870
ID ADL16433 standard; protein; 1117 AA.
DE Human 282P1G3 polypeptide #4.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1117;
Best Local Similarity 25.6%; Pred. No. 2.1e-10;
RESULT 871
ID ADL16592 standard; protein; 1117 AA.
DE Human 282P1G3 polypeptide #39.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1117;
Best Local Similarity 25.6%; Pred. No. 2.1e-10;
RESULT 872
ID ABM83685 standard; protein; 1171 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO.3934.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.7%; Score 229.5; DB 8; Length 1171;
Best Local Similarity 25.6%; Pred. No. 2.2e-10;
RESULT 873
ID ADL16604 standard; protein; 1183 AA.
DE Human 282P1G3 polypeptide #45.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1183;
Best Local Similarity 25.6%; Pred. No. 2.3e-10;
RESULT 874
ID ADL16628 standard; protein; 1183 AA.
DE Human 282P1G3 polypeptide #60.
PN WO2004016734-A2.

PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1183;
Best Local Similarity 25.6%; Pred. No. 2.3e-10;
RESULT 875
ID ADL16449 standard; protein; 1183 AA.
DE Human 282PIG3 polypeptide #15.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1183;
Best Local Similarity 25.6%; Pred. No. 2.3e-10;
RESULT 876
ID ADL16602 standard; protein; 1183 AA.
DE Human 282PIG3 polypeptide #43.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1183;
Best Local Similarity 25.6%; Pred. No. 2.3e-10;
RESULT 877
ID ADL16437 standard; protein; 1183 AA.
DE Human 282PIG3 polypeptide #6.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1183;
Best Local Similarity 25.6%; Pred. No. 2.3e-10;
RESULT 878
ID ADL16448 standard; protein; 1208 AA.
DE Human 282PIG3 polypeptide #14.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1208;
Best Local Similarity 25.6%; Pred. No. 2.3e-10;
RESULT 879
ID ADL16596 standard; protein; 1208 AA.
DE Human 282PIG3 polypeptide #40.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1208;
Best Local Similarity 25.6%; Pred. No. 2.3e-10;
RESULT 880
ID ADL16435 standard; protein; 1208 AA.
DE Human 282PIG3 polypeptide #5.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1208;
Best Local Similarity 25.6%; Pred. No. 2.3e-10;
RESULT 881
ID ADL16627 standard; protein; 1208 AA.
DE Human 282PIG3 polypeptide #59.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1208;
Best Local Similarity 25.6%; Pred. No. 2.3e-10;
RESULT 882
ID ADL16598 standard; protein; 1208 AA.
DE Human 282PIG3 polypeptide #42.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1208;
Best Local Similarity 25.6%; Pred. No. 2.3e-10;
RESULT 883
ID ADL16457 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #23.
PN WO2004016734-A2.
PD 23-OCT-2003.

PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INSR AGR RES.
Query Match 12.7%; Score 229.5; DB 7; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 884
ID ADL16443 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #9.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 885
ID ADL16597 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #41.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 886
ID ADL16621 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #53.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 887
ID ADL16452 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #18.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 888
ID ADL16623 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #55.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 889
ID ADL16579 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #32.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 890
ID ADL16427 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #1.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 891
ID ADL16455 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #21.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 12.7%; Score 229.5; DB 8; Length 1224;
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 892
ID ADL16457 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #23.
PN WO2004016734-A2.
PD 26-FEB-2004.

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PA (AGEN-) AGENSYS INC. 12.7%; Score 229.5; DB 8; Length 1224;
Query Match
Best Local Similarity 25.6%; Pred. No. 2.4e-10;
RESULT 893
ID ADL16591 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #38.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 12.7%; Score 229.5; DB 8; Length 1224;
RESULT 894
ID ADL16620 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #52.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 12.7%; Score 229.5; DB 8; Length 1224;
RESULT 895
ID ADL16456 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #22.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 12.7%; Score 229.5; DB 8; Length 1224;
RESULT 896
ID ADL16615 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #50.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 12.7%; Score 229.5; DB 8; Length 1224;
RESULT 897
ID ADL16622 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #54.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 12.7%; Score 229.5; DB 8; Length 1224;
RESULT 898
ID ADL16444 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #10.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 12.7%; Score 229.5; DB 8; Length 1224;
RESULT 899
ID ADL16458 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #24.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 12.7%; Score 229.5; DB 8; Length 1224;
RESULT 900
ID ADL16550 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #27.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 12.7%; Score 229.5; DB 8; Length 1224;
RESULT 901
ID ADL16459 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #25.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 12.7%; Score 229.5; DB 8; Length 1224;
RESULT 902
ID ADL16603 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #44.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 12.7%; Score 229.5; DB 8; Length 1224;
RESULT 903
ID ADL16453 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #19.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 12.7%; Score 229.5; DB 8; Length 1224;
RESULT 904
ID ADL16632 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #63.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 12.7%; Score 229.5; DB 8; Length 1224;
RESULT 905
ID ADL16609 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #47.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 12.7%; Score 229.5; DB 8; Length 1224;
RESULT 906
ID ADQ39441 standard; protein; 3588 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1104.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 12.7%; Score 229; DB 8; Length 3588;
RESULT 907
ID ADQ39440 standard; protein; 4346 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1103.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 12.7%; Score 229; DB 8; Length 4346;
RESULT 908
ID ADQ39439 standard; protein; 4347 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1102.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 12.7%; Score 229; DB 8; Length 4347;
RESULT 909
ID ADJ69461 standard; protein; 4370 AA.
DE Human heart mitochondrial protein as a therapeutic target SeqID1267.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match
Best Local Similarity 12.7%; Score 229; DB 7; Length 4370;
RESULT 910
ID A6G16336 standard; protein; 1483 AA.
DE Novel human diagnostic protein #16327.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
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Query Match      12.6%; Score 228; DB 4; Length 1483;
Best Local Similarity 24.1%; Pred. No. 4.1e-10;
RESULT 911
ID ADN22360 standard; protein; 6642 AA.
DE Bacterial polypeptide #5013.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match      12.5%; Score 226; DB 8; Length 6642;
Best Local Similarity 23.7%; Pred. No. 4.8e-09;
RESULT 912
ID AAR92718 standard; protein; 478 AA.
DE Mouse muscle-localized protein-tyrosine-kinase receptor 5' fragment.
PN WO9602644-A1.
PD 01-FEB-1996.
PA (GEMV/) GENETICS INST INC.
Query Match      12.5%; Score 225.5; DB 2; Length 478;
Best Local Similarity 24.8%; Pred. No. 1.4e-10;
RESULT 913
ID AAR92716 standard; protein; 860 AA.
DE Mouse muscle-localized protein-tyrosine-kinase receptor-1 isoform.
PN WO9602644-A1.
PD 01-FEB-1996.
PA (GEMV/) GENETICS INST INC.
Query Match      12.5%; Score 225.5; DB 2; Length 860;
Best Local Similarity 24.8%; Pred. No. 3.2e-10;
RESULT 914
ID AAR92717 standard; protein; 868 AA.
DE Mouse muscle-localized protein-tyrosine-kinase receptor-2 isoform.
PN WO9602644-A1.
PD 01-FEB-1996.
PA (GEMV/) GENETICS INST INC.
Query Match      12.5%; Score 225.5; DB 2; Length 868;
Best Local Similarity 24.8%; Pred. No. 3.3e-10;
RESULT 915
ID ABU10922 standard; protein; 869 AA.
DE Human secreted protein (SECP) #18.
PN WO200270669-A2.
PD 12-SEP-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match      12.5%; Score 225.5; DB 5; Length 869;
Best Local Similarity 29.5%; Pred. No. 3.3e-10;
RESULT 916
ID AAE34390 standard; protein; 4391 AA.
DE Human perlecan protein.
PN WO200295415-A2.
PD 28-NOV-2002.
PA (OSTE-) OSTEOMETER BIO TECH AS.
Query Match      12.5%; Score 225; DB 6; Length 4391;
Best Local Similarity 25.7%; Pred. No. 3.3e-09;
RESULT 917
ID ABG74129 standard; protein; 537 AA.
DE Human hMUSK-R deletion mutant mMUSK-RI.
PN US2002150876-A1.
PD 17-OCT-2002.
PA (PIPP/) PIPPIG S D.
PA (VERE/) VERES G.
Query Match      12.4%; Score 224.5; DB 4; Length 537;
Best Local Similarity 26.0%; Pred. No. 2.1e-10;
RESULT 918
ID AAG77857 standard; protein; 537 AA.
DE Mutant protein mMUSK-RI.
PN WO200172834-A1.
PD 04-OCT-2001.
PA (NOVS/) NOVARTIS AG.
PA (NOVS/) NOVARTIS-ERFINDUNGEN VERW GRS MBH.
Query Match      12.4%; Score 224.5; DB 4; Length 537;
Best Local Similarity 26.0%; Pred. No. 2.1e-10;
RESULT 919
ID ABG74130 standard; protein; 576 AA.
DE Human hMUSK-R deletion mutant mMUSK-RI1.
PN US2002150876-A1.
PD 17-OCT-2002.
PA (PIPP/) PIPPIG S D.
PA (VERE/) VERES G.
Query Match      12.4%; Score 224.5; DB 4; Length 576;
Best Local Similarity 26.0%; Pred. No. 2.3e-10;
RESULT 920
ID AAG77858 standard; protein; 576 AA.
DE Mutant protein mMUSK-RI1.
PN WO200172834-A1.
PD 04-OCT-2001.
PA (NOVS/) NOVARTIS AG.
PA (NOVS/) NOVARTIS-ERFINDUNGEN VERW GRS MBH.
Query Match      12.4%; Score 224.5; DB 4; Length 576;
Best Local Similarity 26.0%; Pred. No. 2.3e-10;
RESULT 921
ID ABG74128 standard; protein; 869 AA.
DE Human muscle specific tyrosine kinase receptor, hMUSK-R.
PN US2002150876-A1.
PD 17-OCT-2002.
PA (PIPP/) PIPPIG S D.
PA (VERE/) VERES G.
Query Match      12.4%; Score 224.5; DB 4; Length 869;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 922
ID AAB68421 standard; protein; 869 AA.
DE Amino acid sequence of a human MUSK-R polypeptide.
PN WO200136659-A2.
PD 25-MAY-2001.
PA (NOVS/) NOVARTIS AG.
PA (NOVS/) NOVARTIS-ERFINDUNGEN VERW GRS MBH.
Query Match      12.4%; Score 224.5; DB 4; Length 869;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 923
ID AAG77856 standard; protein; 869 AA.
DE Protein of muscle specific tyrosine kinase receptor (hMUSK-R).
PN WO200172834-A1.
PD 04-OCT-2001.
PA (NOVS/) NOVARTIS AG.
PA (NOVS/) NOVARTIS-ERFINDUNGEN VERW GRS MBH.
Query Match      12.4%; Score 224.5; DB 4; Length 869;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 924
ID ADS17276 standard; protein; 869 AA.
DE Human muscle specific tyrosine kinase receptor (hMUSK-R) protein fragment.
PN US6790614-B1.
PD 14-SEP-2004.
PA (NOVS/) NOVARTIS AG.
Query Match      12.4%; Score 224.5; DB 8; Length 869;
Best Local Similarity 26.0%; Pred. No. 4e-10;
RESULT 925
ID ABG22633 standard; protein; 981 AA.
DE Novel human diagnostic protein #22624.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSR-) HYSER INC.
Query Match      12.4%; Score 224.5; DB 4; Length 981;
Best Local Similarity 23.9%; Pred. No. 4.7e-10;
RESULT 926
ID ADR08740 standard; protein; 1113 AA.
DE Human protein useful for treating neurological disease Seq 2246.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) REAS ASSOC BIOTECHNOLOGY.
Query Match      12.4%; Score 224.5; DB 8; Length 1113;
Best Local Similarity 25.3%; Pred. No. 5.6e-10;
RESULT 927
ID ADL16578 standard; protein; 1171 AA.
DE Human 282P1G3 polypeptide #31.
PN WO2004016734-A2.
PD 26-FEB-2004.

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PA (AGEN-) AGENSYS INC.
 Query Match 12.4%; Score 224.5; DB 8; Length 1171;
 Best Local Similarity 25.3%; Pred. No. 6e-10;
 RESULT 928
 ID ADL16624 standard; protein; 1171 AA.
 DE Human 282PIG3 polypeptide #56.
 PN WO2004016734-A2.
 PD 26-FEB-2004.
 PA (AGEN-) AGENSYS INC.
 Query Match 12.4%; Score 224.5; DB 8; Length 1171;
 Best Local Similarity 25.3%; Pred. No. 6e-10;
 RESULT 929
 ID ADL16580 standard; protein; 1171 AA.
 DE Human 282PIG3 polypeptide #33.
 PN WO2004016734-A2.
 PD 26-FEB-2004.
 PA (AGEN-) AGENSYS INC.
 Query Match 12.4%; Score 224.5; DB 8; Length 1171;
 Best Local Similarity 25.3%; Pred. No. 6e-10;
 RESULT 930
 ID ADL16429 standard; protein; 1171 AA.
 DE Human 282PIG3 polypeptide #2.
 PN WO2004016734-A2.
 PD 26-FEB-2004.
 PA (AGEN-) AGENSYS INC.
 Query Match 12.4%; Score 224.5; DB 8; Length 1171;
 Best Local Similarity 25.3%; Pred. No. 6e-10;
 RESULT 931
 ID ADL16445 standard; protein; 1171 AA.
 DE Human 282PIG3 polypeptide #11.
 PN WO2004016734-A2.
 PD 26-FEB-2004.
 PA (AGEN-) AGENSYS INC.
 Query Match 12.4%; Score 224.5; DB 8; Length 1171;
 Best Local Similarity 25.3%; Pred. No. 6e-10;
 RESULT 932
 ID ADE5536 standard; protein; 1224 AA.
 DE Human Protein AAB60937, SEQ ID NO 1049.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GENO) GEN HOSPITAL CORP.
 Query Match 12.4%; Score 224.5; DB 7; Length 1224;
 Best Local Similarity 25.3%; Pred. No. 6.4e-10;
 RESULT 933
 ID ADL15032 standard; protein; 1224 AA.
 DE Human neural cell adhesion molecule protein for cancer treatment.
 PN WO2003068268-A2.
 PD 21-AUG-2003.
 PA (BIOT-) BIOINVENT INT AB.
 Query Match 12.4%; Score 224.5; DB 7; Length 1224;
 Best Local Similarity 25.3%; Pred. No. 6.4e-10;
 RESULT 934
 ID ADJ75519 standard; protein; 1224 AA.
 DE Marker gene related amino acid sequence SEQ ID NO:771.
 PN EP1394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INC.
 Query Match 12.4%; Score 224.5; DB 8; Length 1224;
 Best Local Similarity 25.3%; Pred. No. 6.4e-10;
 RESULT 935
 ID ADL16454 standard; protein; 1224 AA.
 DE Human 282PIG3 polypeptide #20.
 PN WO2004016734-A2.
 PD 26-FEB-2004.
 PA (AGEN-) AGENSYS INC.
 Query Match 12.4%; Score 224.5; DB 8; Length 1224;
 Best Local Similarity 25.3%; Pred. No. 6.4e-10;
 RESULT 936
 ID ADN04062 standard; protein; 1224 AA.
 DE Antiposoriatic protein sequence #226.
 PN WO2004028479-A2.
 PD 08-APR-2004.

PA (GENE) GENENTECH INC.
 Query Match 12.4%; Score 224.5; DB 8; Length 1224;
 Best Local Similarity 25.3%; Pred. No. 6.4e-10;
 RESULT 937
 ID ADO19766 standard; protein; 1224 AA.
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2585.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 12.4%; Score 224.5; DB 8; Length 1224;
 Best Local Similarity 25.3%; Pred. No. 6.4e-10;
 RESULT 938
 ID ADRL4776 standard; protein; 1224 AA.
 DE Amino acid sequence of human MAPKAPK orthologue #8.
 PN WO2004066948-A2.
 PD 12-AUG-2004.
 PA (EXEL-) EXELIXIS INC.
 Query Match 12.4%; Score 224.5; DB 8; Length 1224;
 Best Local Similarity 25.3%; Pred. No. 6.4e-10;
 RESULT 939
 ID ADP29420 standard; protein; 1583 AA.
 DE Human secreted protein SEQ ID #187.
 PN WO2004035732-A2.
 PD 29-APR-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 12.4%; Score 224.5; DB 8; Length 1583;
 Best Local Similarity 23.9%; Pred. No. 9.1e-10;
 RESULT 940
 ID ADP29354 standard; protein; 1583 AA.
 DE Human secreted protein SEQ ID #121.
 PN WO2004035732-A2.
 PD 29-APR-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 12.4%; Score 224.5; DB 8; Length 1583;
 Best Local Similarity 23.9%; Pred. No. 9.1e-10;
 RESULT 941
 ID ABG20008 standard; protein; 1645 AA.
 DE Novel human diagnostic protein #19999.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 12.4%; Score 224.5; DB 4; Length 1645;
 Best Local Similarity 23.9%; Pred. No. 9.5e-10;
 RESULT 942
 ID ABG22631 standard; protein; 1765 AA.
 DE Novel human diagnostic protein #22622.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 12.4%; Score 224.5; DB 4; Length 1765;
 Best Local Similarity 23.9%; Pred. No. 1.1e-09;
 RESULT 943
 ID ABG12017 standard; protein; 1944 AA.
 DE Novel human diagnostic protein #12008.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 12.4%; Score 224.5; DB 4; Length 1944;
 Best Local Similarity 23.9%; Pred. No. 1.2e-09;
 RESULT 944
 ID AAE30259 standard; peptide; 68 AA.
 DE Human LPZ89 protein immunoglobulin-like domain #1.
 PN WO200274906-A2.
 PD 26-SEP-2002.
 PA (ELIT) LILLY & CO ELI.
 Query Match 12.4%; Score 224; DB 6; Length 68;
 Best Local Similarity 65.7%; Pred. No. 1.4e-11;
 RESULT 945
 ID ABG02117 standard; protein; 434 AA.
 DE Novel human diagnostic protein #2108.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.

Query Match 12.4%; Score 224; DB 4; Length 434;
Best Local Similarity 25.5%; Pred. No. 1.7e-10;
RESULT 946
ID AAM93829 standard; protein; 697 AA.
DE Human polypeptide, SEQ ID NO: 3893.
PN EPI130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 12.4%; Score 224; DB 4; Length 697;
Best Local Similarity 23.9%; Pred. No. 3.3e-10;
RESULT 947
ID ADJ1860 standard; protein; 697 AA.
DE Human protein encoded by a full length cDNA clone seqID 3893.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.4%; Score 224; DB 8; Length 697;
Best Local Similarity 23.9%; Pred. No. 3.3e-10;
RESULT 948
ID ABG02019 standard; protein; 737 AA.
DE Novel human diagnostic protein #2010.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 224; DB 4; Length 737;
Best Local Similarity 25.5%; Pred. No. 3.5e-10;
RESULT 949
ID AAY08095 standard; protein; 1059 AA.
DE Human PRO335 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 2; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 950
ID AAY13393 standard; protein; 1059 AA.
DE Amino acid sequence of protein PRO335.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 2; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 951
ID AAY70672 standard; protein; 1059 AA.
DE Human PRO335 protein.
PN WO200015797-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 3; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 952
ID ADC78602 standard; protein; 1059 AA.
DE Human PRO335 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 3; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 953
ID AAB80261 standard; protein; 1059 AA.
DE Human PRO335 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 4; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 954
ID AAU00825 standard; protein; 1059 AA.
DE Human immune response protein PRO335 (UNQ287).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 4; Length 1059;

Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 955
ID ABU71639 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 956
ID ABU71494 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 957
ID ABU71940 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein PRO335.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 958
ID AB001823 standard; protein; 1059 AA.
DE Novel human secreted and transmembrane protein PRO335.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 959
ID ABUS4396 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein PRO335.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 960
ID AB047411 standard; protein; 1059 AA.
DE Human secreted/transmembrane polypeptide PRO335.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 961
ID ABU64548 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #52.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 962
ID ABU67394 standard; protein; 1059 AA.
DE Human secreted protein PRO335.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 963
ID AB014914 standard; protein; 1059 AA.
DE Human secreted / transmembrane polypeptide PRO335.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;

RESULT 964
ID ABO69671 standard; protein; 1059 AA.
DE Novel human secreted and transmembrane protein PRO335.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 965
ID ABO14853 standard; protein; 1059 AA.
DE Human secreted / transmembrane polypeptide PRO335.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 966
ID ADB29495 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 967
ID ADA18351 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 968
ID ABO32805 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein PRO335.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 969
ID ABO34865 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 970
ID ADA16326 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 971
ID ADA42471 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 972
ID ABO17543 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 973

ID ADA16750 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 974
ID ADA13179 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 975
ID ADA42047 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 976
ID ADA17394 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 977
ID ADA42897 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 978
ID ABO17604 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 979
ID ADB77816 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 980
ID ADB74952 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 981
ID ADC28598 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 982
ID ADC39798 standard; protein; 1059 AA.

DE Human secreted/transmembrane protein, #54.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 983
ID ADC40312 standard; protein, 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 984
ID ADC19136 standard; protein, 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 985
ID ADC34436 standard; protein, 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 986
ID ADC29491 standard; protein, 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 987
ID ADC29022 standard; protein, 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 988
ID ADC40907 standard; protein, 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 989
ID ADC19564 standard; protein, 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 990
ID ADC34012 standard; protein, 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 991
ID ADC13082 standard; protein, 1059 AA.
DE Human secreted/transmembrane protein, #54.

PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 992
ID ADC12534 standard; protein, 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 993
ID ADD05089 standard; protein, 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 994
ID ADD04095 standard; protein, 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 995
ID ADD03671 standard; protein, 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 996
ID ADE34923 standard; protein, 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 997
ID ADE59406 standard; protein, 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 998
ID ADI38185 standard; protein, 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 999
ID ADI26453 standard; protein, 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1000
ID ADE79368 standard; protein, 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003135025-A1.

PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1001
ID ADE79792 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1002
ID ADE73468 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1003
ID ADE74003 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1004
ID ADE99557 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1005
ID ADE98676 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1006
ID ADE99103 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1007
ID ADG40573 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1008
ID ADF73967 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;

Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1009
ID ADF73543 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1010
ID ADG92386 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1011
ID ADG92813 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1012
ID ADH20602 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1013
ID ADH07457 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1014
ID ADH60002 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1015
ID ADH07030 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1016
ID ADI18772 standard; protein; 1059 AA.
DE Human secreted/transmembrane protein, #54.
PN US2003152999-A1.

PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1017
ID ADI65492 standard; protein; 1059 AA.
DE Human secreted/cranmembrane protein, #54.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1018
ID ADI37751 standard; protein; 1059 AA.
DE Human secreted/cranmembrane protein, #54.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1019
ID ADH97551 standard; protein; 1059 AA.
DE Human secreted/cranmembrane protein, #54.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1020
ID ADI65919 standard; protein; 1059 AA.
DE Human secreted/cranmembrane protein, #54.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1021
ID ADH60662 standard; protein; 1059 AA.
DE Human secreted/cranmembrane protein, #54.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN) DESNOYERS L.
PA (GODO) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GURN) GURNEY A L.
PA (MATH) MATHER J P.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1022
ID ADI99719 standard; protein; 1059 AA.
DE Human secreted/cranmembrane protein, #54.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1023
ID ADI08912 standard; protein; 1059 AA.
DE Human secreted/cranmembrane protein, #54.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1024
ID ADM25253 standard; protein; 1059 AA.
DE Human secreted/cranmembrane protein, #54.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1025
ID ADM30003 standard; protein; 1059 AA.
DE Human secreted/cranmembrane protein, #54.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1026
ID ADO06325 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1027
ID ADR11177 standard; protein; 1059 AA.
DE Human secreted/cranmembrane protein, #54.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1028
ID ADR18086 standard; protein; 1059 AA.
DE Human secreted/cranmembrane protein, #54.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK) ASHKENAZI A.
PA (BOTS) BOTSTEIN D.
PA (DESN) DESNOYERS L.
PA (EATO) EATON D L.
PA (FERR) FERRARA N.
PA (FILV) FILVAROFF E.
PA (FONG) FONG S.
PA (GAOW) GAO W.
PA (GERB) GERBER H.
PA (GERR) GERRITSEN M E.
PA (GODO) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GRIM) GRIMALDI C J.
PA (GURN) GURNEY A L.
PA (HILL) HILLAN K J.
PA (KJLA) KJAVIN I J.
PA (MATH) MATHER J P.
PA (PANJ) PAN J.
PA (PAON) PAONI N F.
PA (ROYM) ROY M A.
PA (STEW) STEWART T A.
PA (TOMA) TOMAS D.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1029
ID ADT03762 standard; protein; 1059 AA.
DE Human secreted/cranmembrane protein, #54.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1030
ID ADS74725 standard; protein; 1059 AA.
DE Human secreted/cranmembrane protein #54.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK) ASHKENAZI A.
PA (BOTS) BOTSTEIN D.
PA (DESN) DESNOYERS L.
PA (EATO) EATON D L.

Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1025
ID ADM30003 standard; protein; 1059 AA.
DE Human secreted/cranmembrane protein, #54.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1026
ID ADO06325 standard; protein; 1059 AA.
DE Human PRO polypeptide #50.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1027
ID ADR11177 standard; protein; 1059 AA.
DE Human secreted/cranmembrane protein, #54.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1028
ID ADR18086 standard; protein; 1059 AA.
DE Human secreted/cranmembrane protein, #54.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK) ASHKENAZI A.
PA (BOTS) BOTSTEIN D.
PA (DESN) DESNOYERS L.
PA (EATO) EATON D L.
PA (FERR) FERRARA N.
PA (FILV) FILVAROFF E.
PA (FONG) FONG S.
PA (GAOW) GAO W.
PA (GERB) GERBER H.
PA (GERR) GERRITSEN M E.
PA (GODO) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GRIM) GRIMALDI C J.
PA (GURN) GURNEY A L.
PA (HILL) HILLAN K J.
PA (KJLA) KJAVIN I J.
PA (MATH) MATHER J P.
PA (PANJ) PAN J.
PA (PAON) PAONI N F.
PA (ROYM) ROY M A.
PA (STEW) STEWART T A.
PA (TOMA) TOMAS D.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1029
ID ADT03762 standard; protein; 1059 AA.
DE Human secreted/cranmembrane protein, #54.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1030
ID ADS74725 standard; protein; 1059 AA.
DE Human secreted/cranmembrane protein #54.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK) ASHKENAZI A.
PA (BOTS) BOTSTEIN D.
PA (DESN) DESNOYERS L.
PA (EATO) EATON D L.

PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEM/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1059;
Best Local Similarity 23.9%; Pred. No. 5.8e-10;
RESULT 1031
ID AAY08114 standard; protein; 1119 AA.
DE Human PRO326 protein.
PN WO914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 2; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1032
ID AAY70674 standard; protein; 1119 AA.
DE Human PRO326 protein.
PN WO200015797-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 3; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1033
ID ADC78606 standard; protein; 1119 AA.
DE Human PRO326 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 3; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1034
ID AAB80263 standard; protein; 1119 AA.
DE Human PRO326 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 4; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1035
ID AAB48162 standard; protein; 1119 AA.
DE Human PRO326 polypeptide.
PN WO200075316-A1.
PD 14-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 4; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1036
ID AAU00827 standard; protein; 1119 AA.
DE Human immune response protein PRO326 (UNQ287).
PN WO200119891-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 4; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1037
ID AAU12347 standard; protein; 1119 AA.
DE Human PRO326 polypeptide sequence.

PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 4; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1038
ID ABU71641 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1039
ID ABO17791 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1040
ID ABU71496 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1041
ID ABU81045 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1042
ID ABU71942 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein PRO326.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1043
ID ABO01825 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1044
ID ABU66745 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1045
ID ABU54398 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein PRO326.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1046
ID ABO47413 standard; protein; 1119 AA.
DE Human secreted/transmembrane polypeptide PRO326.
PN US2003044839-A1.

PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1047
ID ADB59826 standard; protein; 1119 AA.
DE Novel secreted and transmembrane protein PRO326.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1048
ID ABO25016 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein (PRO) #176.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1049
ID ABB64550 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #54.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1050
ID ABB67396 standard; protein; 1119 AA.
DE Human secreted protein PRO326.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1051
ID ABO14916 standard; protein; 1119 AA.
DE Human secreted / transmembrane polypeptide PRO326.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1052
ID ABB67021 standard; protein; 1119 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 352.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1053
ID ABB69673 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1054
ID ABO14855 standard; protein; 1119 AA.
DE Human secreted / transmembrane polypeptide PRO326.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1055
ID ADA45871 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003022328-A1.
PD 30-JAN-2003.

PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1056
ID ADA76302 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1057
ID ADB29499 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1058
ID ADA18952 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1059
ID ADA61575 standard; protein; 1119 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1060
ID ADB19360 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1061
ID ADB27901 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1062
ID ADA86380 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1063
ID ADB15944 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1064
ID ADA47730 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.


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RESULT 1083
ID ABO43324 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1084
ID ADA74478 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1085
ID ADA42475 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1086
ID ADB2471 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US200307713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1087
ID ADA82235 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1088
ID ADA75198 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1089
ID ADA85276 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1090
ID ADA84724 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1091
ID ABO17545 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1092
ID ADB24159 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1093
ID ADA80508 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1094
ID ADA75750 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1095
ID ADA46975 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1096
ID ADB25271 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US200307715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1097
ID ADA93447 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US200307721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1098
ID ADB26797 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1099
ID ADB31084 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1100
ID ADA61012 standard; protein; 1119 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1101
ID ADB24159 standard; protein; 1119 AA.
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DE Human PRO polypeptide SEQ ID NO 352.
PN US200307714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1102
ID ADA96488 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1103
ID ADA81060 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1104
ID ADA95936 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1105
ID ADB26245 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1106
ID ADB21730 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 6; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1107
ID ADA77509 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003086797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1108
ID ADB18249 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US200307710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1109
ID ADA86932 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1110
ID ADA16754 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.

PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1111
ID ADA13183 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1112
ID ADA42051 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1113
ID ADA86035 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1114
ID ADA46423 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1115
ID ADA17398 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1116
ID ADA42901 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1117
ID ADB28453 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1118
ID ADB29005 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1119
ID ADA76957 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.

PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1120
ID ADA88587 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1121
ID ADA97592 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1122
ID ADB27349 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1123
ID ADB22282 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1124
ID ABO17606 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1125
ID ADA66973 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1126
ID ADB22834 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1127
ID ADB23607 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1128
ID ADB92329 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;

Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1129
ID ADB15392 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1130
ID ADB38644 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1131
ID ADB38092 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1132
ID ADB6564 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1133
ID ADB89644 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1134
ID ADB90376 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1135
ID ADB77820 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1136
ID ADB39477 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1137
ID ADB74956 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;

RESULT 1138
ID ADB47100 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1139
ID ADB86707 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1140
ID ADB77312 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1141
ID ADB34469 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1142
ID ADB35573 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1143
ID ADB33917 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1144
ID ADB35021 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1145
ID ADB36125 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1146
ID ADB45520 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1147

ID ADC28602 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1148
ID ADC39802 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1149
ID ADC40316 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1150
ID ADC19140 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1151
ID ADC34440 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1152
ID ADC29495 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1153
ID ADC29026 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1154
ID ADC40911 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1155
ID ADC19568 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1156
ID ADC34016 standard; protein; 1119 AA.

DE Human secreted/transmembrane protein, #56.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1157
ID ADC13086 standard; protein, 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1158
ID ADC50393 standard; protein, 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1159
ID ADC71940 standard; protein, 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1160
ID ADC59919 standard; protein, 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1161
ID ADC52926 standard; protein, 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1162
ID ADC57280 standard; protein, 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1163
ID ADC60471 standard; protein, 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1164
ID ADC50946 standard; protein, 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1165
ID ADC65473 standard; protein, 1119 AA.
DE Human PRO polypeptide #176.

PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1166
ID ADC54571 standard; protein, 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1167
ID ADC53532 standard; protein, 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1168
ID ADC59055 standard; protein, 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1169
ID ADC55933 standard; protein, 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1170
ID ADC58503 standard; protein, 1119 AA.
DE Novel human secreted and transmembrane protein Seq ID352.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1171
ID ADC12538 standard; protein, 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1172
ID ADD03177 standard; protein, 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1173
ID ADC90169 standard; protein, 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1174
ID ADC69588 standard; protein, 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194770-A1.

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PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1175
ID ADC48477 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1176
ID ADD10006 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1177
ID ADD04581 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1178
ID ADC80537 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1179
ID ADD11044 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1180
ID ADC47925 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1181
ID ADD05093 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1182
ID ADC79985 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1183
ID ADD09454 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1184
ID ADD04099 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1185
ID ADD03675 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1186
ID ADD4167 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1187
ID ADD52306 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1188
ID ADD53046 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1189
ID ADD53598 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1190
ID ADD51754 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1191
ID ADD02553 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1192
ID ADD01987 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
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RESULT 1211
ID ADE95891 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1212
ID ADE22777 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003198064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1213
ID ADE76895 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1214
ID ADE32845 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1215
ID ADE42537 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003198032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1216
ID ADE80553 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1217
ID ADE89581 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1218
ID ADE40865 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003198031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1219
ID ADE04664 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1220

ID ADE92793 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1221
ID ADE21502 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1222
ID ADE23143 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1223
ID ADE97478 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1224
ID ADE80542 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1225
ID ADE79990 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1226
ID ADE59410 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1227
ID ADE55282 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1228
ID ADE55834 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1229
ID ADE18189 standard; protein; 1119 AA.

DE Human secreted/transmembrane protein, #56.
 PN US200305432-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 7; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1230
 ID ADI64053 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2003207385-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 7; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1231
 ID ADI65002 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2003207386-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 7; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1232
 ID ADI63501 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2003207387-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 7; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1233
 ID ADH81915 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2003207388-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 7; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1234
 ID ADH81363 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2003207377-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 7; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1235
 ID ADJ26457 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2003054349-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 7; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1236
 ID ADH82532 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2003087355-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 7; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1237
 ID ADN15931 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2003087353-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 7; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1238
 ID ADN16560 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.

PN US2003087385-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 7; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1239
 ID ADN15379 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2003087356-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 7; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1240
 ID ADN14827 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2003087357-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 7; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1241
 ID ADC81089 standard; protein; 1119 AA.
 DE Novel human secreted and transmembrane protein PRO326.
 PN US2003092115-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1242
 ID ADE79372 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2003135025-A1.
 PD 17-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1243
 ID ADD76537 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2003100087-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1244
 ID ADD87901 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2003092113-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1245
 ID ADD86305 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2003203440-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1246
 ID ADE79796 standard; protein; 1119 AA.
 DE Human secreted/transmembrane protein, #56.
 PN US2003130489-A1.
 PD 10-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 12.4%; Score 224; DB 8; Length 1119;
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;
 RESULT 1247
 ID ADE75753 standard; protein; 1119 AA.
 DE Human PRO polypeptide #176.
 PN US2003211571-A1.

PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1248
ID ADEB73472 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1249
ID ADEB23329 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1250
ID ADEB23881 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1251
ID ADEB24524 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1252
ID ADEB7349 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1253
ID ADEB89215 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1254
ID ADEB74007 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1255
ID ADEB18354 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1256
ID ADEB8663 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199054-A1.
PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1257
ID ADEB9561 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1258
ID ADEB94683 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1259
ID ADEB91094 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1260
ID ADEB95235 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1261
ID ADEB93345 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1262
ID ADF34926 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1263
ID ADEB96680 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1264
ID ADEB92241 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1265
ID ADEB90542 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

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Query Match 12.4% Score 224; DB 8; Length 1119;
Best Local Similarity 23.9% Pred. No. 6.2e-10;
RESULT 1266
ID ADP91689 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US200319058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4% Score 224; DB 8; Length 1119;
Best Local Similarity 23.9% Pred. No. 6.2e-10;
RESULT 1267
ID ADP99107 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4% Score 224; DB 8; Length 1119;
Best Local Similarity 23.9% Pred. No. 6.2e-10;
RESULT 1268
ID ADG40577 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATR/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4% Score 224; DB 8; Length 1119;
Best Local Similarity 23.9% Pred. No. 6.2e-10;
RESULT 1269
ID ADP73971 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4% Score 224; DB 8; Length 1119;
Best Local Similarity 23.9% Pred. No. 6.2e-10;
RESULT 1270
ID ADG02268 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4% Score 224; DB 8; Length 1119;
Best Local Similarity 23.9% Pred. No. 6.2e-10;
RESULT 1271
ID ADG22054 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4% Score 224; DB 8; Length 1119;
Best Local Similarity 23.9% Pred. No. 6.2e-10;
RESULT 1272
ID ADG20124 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4% Score 224; DB 8; Length 1119;
Best Local Similarity 23.9% Pred. No. 6.2e-10;
RESULT 1273
ID ADP98030 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4% Score 224; DB 8; Length 1119;
Best Local Similarity 23.9% Pred. No. 6.2e-10;
RESULT 1274
ID ADG08358 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4% Score 224; DB 8; Length 1119;
Best Local Similarity 23.9% Pred. No. 6.2e-10;
RESULT 1275
ID ADP98601 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4% Score 224; DB 8; Length 1119;
Best Local Similarity 23.9% Pred. No. 6.2e-10;
RESULT 1276
ID ADG03432 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4% Score 224; DB 8; Length 1119;
Best Local Similarity 23.9% Pred. No. 6.2e-10;
RESULT 1277
ID ADP99153 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4% Score 224; DB 8; Length 1119;
Best Local Similarity 23.9% Pred. No. 6.2e-10;
RESULT 1278
ID ADG16773 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4% Score 224; DB 8; Length 1119;
Best Local Similarity 23.9% Pred. No. 6.2e-10;
RESULT 1279
ID ADG05197 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4% Score 224; DB 8; Length 1119;
Best Local Similarity 23.9% Pred. No. 6.2e-10;
RESULT 1280
ID ADG19464 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4% Score 224; DB 8; Length 1119;
Best Local Similarity 23.9% Pred. No. 6.2e-10;
RESULT 1281
ID ADP73547 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4% Score 224; DB 8; Length 1119;
Best Local Similarity 23.9% Pred. No. 6.2e-10;
RESULT 1282
ID ADG13301 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4% Score 224; DB 8; Length 1119;
Best Local Similarity 23.9% Pred. No. 6.2e-10;
RESULT 1283
ID ADG08358 standard; protein; 1119 AA.
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DE Novel human secreted and transmembrane protein PRO326.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1284
ID ADG15528 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1285
ID ADF66926 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1286
ID ADG06111 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1287
ID ADG23695 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1288
ID ADG03984 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1289
ID ADG24885 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1290
ID ADG07182 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1291
ID ADG07734 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1292
ID ADG55229 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.

PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1293
ID ADG60893 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1294
ID ADG61997 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1295
ID ADG92390 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1296
ID ADG82198 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1297
ID ADG57437 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1298
ID ADG56885 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1299
ID ADG55781 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1300
ID ADG58541 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1301
ID ADG70907 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207420-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1302
ID ADG92817 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1303
ID ADG57989 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1304
ID ADG53573 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1305
ID ADG71459 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1306
ID ADG81646 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1307
ID ADH30608 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1308
ID ADH11975 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1309
ID ADG52397 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1310
ID ADG54125 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1311
ID ADG81094 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1312
ID ADG56333 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1313
ID ADH12599 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1314
ID ADG61445 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1315
ID ADH28532 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1316
ID ADG54677 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1317
ID ADG59717 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1318
ID ADH20606 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1319
ID ADH07461 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.

PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1320
ID ADH6006 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1321
ID ADH07034 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1322
ID ADI8141 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1323
ID ADI1876 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1324
ID ADI37755 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1325
ID ADG09884 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1326
ID ADH97555 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1327
ID ADI1535 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207382-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1328
ID ADG09232 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1329
ID ADI65923 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1330
ID ADI14687 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1331
ID ADH60666 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1332
ID ADI18282 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1333
ID ADJ99723 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1334
ID ADL08916 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1335
ID ADM25257 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;

Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1336
ID ADJ63563 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1337
ID ADM30007 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1338
ID ADJ77458 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1339
ID ADJ65580 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1340
ID ADM27716 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1341
ID ADM42440 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1342
ID ADO06329 standard; protein; 1119 AA.
DE Human PRO polypeptide #52.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1343
ID ADM28302 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1344
ID ADRI1181 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;

RESULT 1345
ID ADRI8090 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANU/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1346
ID ADI95784 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US200307659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1347
ID ADI96336 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1348
ID ADT03766 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003152822-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.4%; Score 224; DB 8; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1349
ID ADS74729 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein #56.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.

PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEM/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 12.4%; Score 224; DB 8; Length 1119;
RESULT 1350
ID ADA55073 standard; protein; 1251 AA.
DE Human protein, SEQ ID 2641.
PN EPI293569-A2.
PD 19-MAR-2003.
PA (HELT-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 12.4%; Score 224; DB 6; Length 1251;
RESULT 1351
ID ABU11674 standard; protein; 380 AA.
DE Human MDT polypeptide SEQ ID 621.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 12.3%; Score 223; DB 6; Length 380;
RESULT 1352
ID AAV53028 standard; protein; 414 AA.
DE Human secreted protein clone cw1000_2 protein sequence SEQ ID NO:62.
PN WO9957133-A1.
PD 11-NOV-1999.
PA (GEMY) GENETICS INST. INC.
Query Match
Best Local Similarity 12.3%; Score 223; DB 3; Length 414;
RESULT 1353
ID ABJ20228 standard; protein; 798 AA.
DE Human IG gene related protein SEQ ID No 51.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 12.3%; Score 223; DB 6; Length 798;
RESULT 1354
ID ABB97578 standard; protein; 1179 AA.
DE Novel human protein SEQ ID NO: 846.
PN WO200222860-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.3%; Score 223; DB 5; Length 1179;
RESULT 1355
ID ADR28014 standard; protein; 1179 AA.
DE Long form IGSF9 protein.
PN WO2004066933-A2.
PD 12-AUG-2004.
PA (MCLA/) MCLACHLAN K.
PA (GLAS/) GLASER S.
PA (PEAC/) PEACH R J.
PA (ROWE/) ROWE T.
Query Match
Best Local Similarity 12.3%; Score 223; DB 8; Length 1179;
RESULT 1356
ID ABR28013 standard; protein; 1179 AA.
DE Long form full-length IGSF9 protein.
PN WO2004066933-A2.
PD 12-AUG-2004.
PA (MCLA/) MCLACHLAN K.
PA (GLAS/) GLASER S.
PA (PEAC/) PEACH R J.

PA (ROWE/) ROWE T.
Query Match
Best Local Similarity 12.3%; Score 223; DB 8; Length 1179;
RESULT 1357
ID ADR09753 standard; protein; 595 AA.
DE Human protein useful for treating neurological disease Seq 3259.
PN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 12.3%; Score 222; DB 8; Length 595;
RESULT 1358
ID ABR10202 standard; protein; 744 AA.
DE Human cDNA SEQ ID NO: 510.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 12.3%; Score 222; DB 4; Length 744;
RESULT 1359
ID ABP66789 standard; protein; 744 AA.
DE Human polypeptide SEQ ID NO 510.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 12.3%; Score 222; DB 5; Length 744;
RESULT 1360
ID ADH72194 standard; protein; 1068 AA.
DE Human protein of the invention NOV51d SEQ ID NO:1090.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 12.3%; Score 222; DB 8; Length 1068;
RESULT 1361
ID AAW42087 standard; protein; 1571 AA.
DE Human Down syndrome-cell adhesion molecule DS-CAM2.
PN WO9817795-A1.
PD 30-APR-1998.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
Query Match
Best Local Similarity 12.2%; Score 221; DB 2; Length 1571;
RESULT 1362
ID AAW42086 standard; protein; 1910 AA.
DE Human Down syndrome-cell adhesion molecule DS-CAM1.
PN WO9817795-A1.
PD 30-APR-1998.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
Query Match
Best Local Similarity 12.2%; Score 221; DB 2; Length 1910;
RESULT 1363
ID ADK71092 standard; protein; 2012 AA.
DE Human MP21 polypeptide.
PN WO2004015073-A2.
PD 19-FEB-2004.
PA (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 12.2%; Score 221; DB 8; Length 2012;
RESULT 1364
ID AAB25586 standard; protein; 364 AA.
DE Protein encoded by human secreted protein gene #11.
PN WO200029435-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 3; Length 364;
RESULT 1365
ID ADA27058 standard; protein; 364 AA.
DE Human novel secreted protein from cDNA HOU0J81 #1.
PN US2003055231-A1.

PD	20-MAR-2003.
PA	(NITJ/) NI J.
PA	(YOUN/) YOUNG P E.
PA	(KENN/) KENNY J U.
PA	(OLSE/) OLSEN H S.
PA	(MOOR/) MOORE P A.
PA	(WEIY/) WEI Y.
PA	(GREB/) GREENE J M.
PA	(RUBE/) RUBEN S M.
PA	(LITU/) LIT D.
PA	(CRCK/) CROCKER P R.
Query Match	12.2%; Score 220.5; DB 6;
Best Local Similarity	26.0%; Pred. No. 2.7e-10; Length 364;
RESULT 1366	
ID	ADE86598 standard; protein; 364 AA.
DE	Novel human secreted protein #11.
PN	US2003129685-A1.
PD	10-JUL-2003.
PA	(NITJ/) NI J.
PA	(YOUN/) YOUNG P E.
PA	(KENN/) KENNY J U.
PA	(OLSE/) OLSEN H S.
PA	(MOOR/) MOORE P A.
PA	(WEIY/) WEI Y.
PA	(GREB/) GREENE J M.
PA	(RUBE/) RUBEN S M.
Query Match	12.2%; Score 220.5; DB 8;
Best Local Similarity	26.0%; Pred. No. 2.7e-10; Length 364
RESULT 1367	
ID	ADR41469 standard; protein; 370 AA.
DE	Human CD-like molecule HATCZ07, SEQ ID NO:268.
PN	WO200226930-A2.
PD	04-APR-2002.
PA	(HUMA-) HUDAN GENOME SCI INC.
Query Match	12.2%; Score 220.5; DB 5;
Best Local Similarity	26.0%; Pred. No. 2.7e-10; Length 370;
RESULT 1368	
ID	AAM23691 standard; protein; 402 AA.
DE	Human EST encoded protein SEQ ID NO: 1216.
PN	WO200154477-A2.
PD	02-AUG-2001.
PA	(HYSE-) HYSEQ INC.
Query Match	12.2%; Score 220.5; DB 4;
Best Local Similarity	26.0%; Pred. No. 3.1e-10; Length 402;
RESULT 1369	
ID	AAV45093 standard; protein; 423 AA.
DE	Mouse lymphoid derived dendritic cell adhesion molecule.
PN	WO200008156-A2.
PD	17-FEB-2000.
PA	(IMNV) IMMUNEX CORP.
Query Match	12.2%; Score 220.5; DB 3;
Best Local Similarity	26.0%; Pred. No. 3.3e-10; Length 423;
RESULT 1370	
ID	ABO84564 standard; protein; 425 AA.
DE	Human cancer-associated protein HPIc-039.1.
PN	WO2004074320-A2.
PD	02-SEP-2004.
PA	(SAGR-) SAGRES DISCOVERY INC.
Query Match	12.2%; Score 220.5; DB 8;
Best Local Similarity	26.0%; Pred. No. 3.3e-10; Length 425;
RESULT 1371	
ID	AAV17830 standard; protein; 440 AA.
DE	Human PRO355 protein sequence.
PN	WO9928462-A2.
PD	10-JUN-1999.
PA	(GETH) GENEINTECH INC.
Query Match	12.2%; Score 220.5; DB 2;
Best Local Similarity	26.0%; Pred. No. 3.5e-10; Length 440;
RESULT 1372	
ID	AAAB01321 standard; protein; 440 AA.
DE	Human PRO355 polypeptide.
PN	WO200032776-A2.
PD	08-JUN-2000.

PA	(GETH) GENENTECH INC.	12.2%;	Score 220.5;	DB 3;	Length 440;
Query Match					
BE	Beet Local Similarity	26.0%;	Pred. No. 3.5e-10;		
RESULT 1373					
ID	AAU29040 standard; protein; 440 AA.				
DE	Human PRO polypeptide sequence #17.				
FN	WO200168848-A2.				
PD	20-SEP-2001.				
PA	(GETH) GENENTECH INC.				
Query Match		12.2%;	Score 220.5;	DB 4;	Length 440;
BE	Beet Local Similarity	26.0%;	Pred. No. 3.5e-10;		
RESULT 1374					
ID	ABUS8416 standard; protein; 440 AA.				
DE	Human PRO polypeptide #17.				
FN	US2003027272-A1.				
PD	06-FEB-2003.				
Query Match		12.2%;	Score 220.5;	DB 6;	Length 440;
BE	Beet Local Similarity	26.0%;	Pred. No. 3.5e-10;		
RESULT 1375					
ID	ABU87964 standard; protein; 440 AA.				
DE	Novel human secreted and transmembrane protein PRO355.				
FN	US2003032127-A1.				
PD	13-FEB-2003.				
Query Match		12.2%;	Score 220.5;	DB 6;	Length 440;
BE	Beet Local Similarity	26.0%;	Pred. No. 3.5e-10;		
RESULT 1376					
ID	ABU84279 standard; protein; 440 AA.				
DE	Human secreted/transmembrane protein (PRO) #17.				
FN	US2003032112-A1.				
PD	13-FEB-2003.				
Query Match		12.2%;	Score 220.5;	DB 6;	Length 440;
BE	Beet Local Similarity	26.0%;	Pred. No. 3.5e-10;		
RESULT 1377					
ID	ABR6153 standard; protein; 440 AA.				
DE	Human secreted polypeptide PRO355, SEQ ID NO:34.				
FN	US2003027278-A1.				
PD	06-FEB-2003.				
Query Match		12.2%;	Score 220.5;	DB 6;	Length 440;
BE	Beet Local Similarity	26.0%;	Pred. No. 3.5e-10;		
RESULT 1378					
ID	ABR65543 standard; protein; 440 AA.				
DE	Human secreted polypeptide PRO355, SEQ ID NO:134.				
FN	US2003036159-A1.				
PD	20-FEB-2003.				
Query Match		12.2%;	Score 220.5;	DB 6;	Length 440;
BE	Beet Local Similarity	26.0%;	Pred. No. 3.5e-10;		
RESULT 1379					
ID	ABU93943 standard; protein; 440 AA.				
DE	Human secreted/transmembrane protein (PRO) #17.				
FN	US2003040070-A1.				
PD	27-FEB-2003.				
Query Match		12.2%;	Score 220.5;	DB 6;	Length 440;
BE	Beet Local Similarity	26.0%;	Pred. No. 3.5e-10;		
RESULT 1380					
ID	ABUS5930 standard; protein; 440 AA.				
DE	Human secreted/transmembrane protein PRO355.				
FN	US2002142959-A1.				
PD	03-OCT-2002.				
PA	(GETH) GENENTECH INC.				
Query Match		12.2%;	Score 220.5;	DB 6;	Length 440;
BE	Beet Local Similarity	26.0%;	Pred. No. 3.5e-10;		
RESULT 1381					
ID	ABU82722 standard; protein; 440 AA.				
DE	Human PRO polypeptide #17.				
FN	US2003032113-A1.				
PD	13-FEB-2003.				
Query Match		12.2%;	Score 220.5;	DB 6;	Length 440;
BE	Beet Local Similarity	26.0%;	Pred. No. 3.5e-10;		
RESULT 1382					
ID	ABU89843 standard; protein; 440 AA.				
DE	Novel human secreted and transmembrane protein PRO355.				
FN	US2003036147-A1.				
PD	20-FEB-2003.				

Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1383
ID ABR68092 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1384
ID ABU96145 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1385
ID ABU92576 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1386
ID ABO08653 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1387
ID ABO02705 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1388
ID ABR74859 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1389
ID ABR94621 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1390
ID ABU60240 standard; protein; 440 AA.
DE Human PRO polypeptide #11.
PN US2002132768-A1.
PD 19-SEP-2002.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1391
ID ABU85594 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003036140-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1392
ID ABU9754 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;

Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1393
ID ABU97969 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1394
ID ABU91675 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1395
ID ABU89368 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1396
ID ABU86209 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036146-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1397
ID ABU67422 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036162-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1398
ID ABU80450 standard; protein; 440 AA.
DE Human PRO protein #17.
PN US2003036137-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1399
ID ABR99368 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1400
ID ABR98758 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1401
ID ABO16281 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1402
ID ABR92181 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;

Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1403
ID ABO18822 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
RESULT 1404
ID ABR78243 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
RESULT 1405
ID ABR64926 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO355.
PN US2002173463-A1.
PD 21-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
RESULT 1406
ID ABR84979 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
RESULT 1407
ID ABO00118 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
RESULT 1408
ID ABO11450 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
RESULT 1409
ID ABO02095 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
RESULT 1410
ID ABR58360 standard; protein; 440 AA.
DE Novel human secreted protein PRO355.
PN US2002150976-A1.
PD 17-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
RESULT 1411
ID ABR88669 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
RESULT 1412
ID ABR83364 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;

Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1413
ID ABO06165 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US200302294-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
RESULT 1414
ID ABR59201 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
RESULT 1415
ID ABO09263 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
RESULT 1416
ID ABO19127 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
RESULT 1417
ID ABO1145 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
RESULT 1418
ID ABR6763 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
RESULT 1419
ID ABO15976 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
RESULT 1420
ID ABO13682 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
RESULT 1421
ID ABR57246 standard; protein; 440 AA.
DE Human PRO355 protein.
PN US2002142958-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
RESULT 1422
ID ABR65585 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, SEQ ID 34.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;
RESULT 1423
ID ABR65585 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, SEQ ID 34.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;

RESULT 1423
ID ABO07433 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1424
ID ABO03620 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1425
ID ABR67068 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1426
ID ABO15671 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003054483-A1.
PD 20-MAR-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1427
ID ABUS5952 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, PRO355.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1428
ID ABUS65280 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1429
ID ABUS91225 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1430
ID ABU71128 standard; protein; 440 AA.
DE Human PRO355 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1431
ID ABO07738 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1432
ID ABR69979 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003032138-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1433

ID ABR69312 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1434
ID ABO01453 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003008353-A1.
PD 09-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1435
ID ABUS1255 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1436
ID ABR60052 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1437
ID ABR67787 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1438
ID ABR65175 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1439
ID ABR68397 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1440
ID ABR71809 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003032135-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1441
ID ABUS85289 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1442
ID ABUS86979 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1443
ID ABUS3059 standard; protein; 440 AA.

DE Human secreted/transmembrane protein (PRO) #17.
PN US2003032105-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1444
ID AB094915 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1445
ID AB090463 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1446
ID AB083974 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1447
ID AB093625 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032119-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1448
ID AB064870 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1449
ID ABR68702 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1450
ID ABO06518 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1451
ID ABR99063 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1452
ID AB056311 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, PRO355.
PN US2002132981-A1.
PD 19-SEP-2002.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1453
ID AB056947 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1454
ID AB085899 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1455
ID AB082186 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1456
ID AB087197 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1457
ID AB083669 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1458
ID ABO08043 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1459
ID AB060351 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2002168715-A1.
PD 14-NOV-2002.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1460
ID AB081754 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1461
ID AB065918 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1462
ID ABR59747 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1463
ID AB093935 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036155-A1.
PD 20-FEB-2003.

Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1464
ID ABU99788 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1465
ID ABR66458 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1466
ID ABR90876 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1467
ID ABU94303 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1468
ID ABU79185 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1469
ID ABU86514 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1470
ID ABU86819 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1471
ID ABU94608 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1472
ID ABO04535 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1473
ID ABR70284 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1474
ID ABR70894 standard; protein; 440 AA.

RESULT 1474
ID ABU98449 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1475
ID ABR65848 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1476
ID ABR64565 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1477
ID ABU79490 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1478
ID ABU92881 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1479
ID ABU95840 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1480
ID ABU91060 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1481
ID ABU90153 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1482
ID ABO09568 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003046931-A1.
PD 06-MAR-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1483
ID ABO10840 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1484
ID ABR70894 standard; protein; 440 AA.

DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1485
ID AB087502 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1486
ID AB091370 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1487
ID AB084584 standard; protein; 440 AA.
DE Human secreted/cranmembrane protein (PRO) #17.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1488
ID ABR69674 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1489
ID AB080051 standard; protein; 440 AA.
DE Human PRO protein #17.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1490
ID AB093320 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1491
ID AB009873 standard; protein; 440 AA.
DE Human secreted/cranmembrane protein (PRO) #17.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1492
ID AB008958 standard; protein; 440 AA.
DE Human secreted/cranmembrane protein (PRO) #17.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1493
ID AB010526 standard; protein; 440 AA.
DE Human secreted/cranmembrane protein #17.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1494
ID AB011312 standard; protein; 440 AA.
DE Human PRO355 protein sequence.
PN US2002127643-A1.

PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1495
ID AB067131 standard; protein; 440 AA.
DE Human PRO polypeptide #11.
PN US2002165143-A1.
PD 07-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1496
ID AB095535 standard; protein; 440 AA.
DE Human PRO polypeptide #17.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1497
ID AB096744 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1498
ID ABR70589 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1499
ID AB004940 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;
RESULT 1500
ID AB008348 standard; protein; 440 AA.
DE Human secreted/cranmembrane protein (PRO) #17.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 12.2%; Score 220.5; DB 6; Length 440;
Best Local Similarity 26.0%; Pred. No. 3.5e-10;

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